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Sequence 11, Appl Sequence 11, Appl Sequence 21, Appl Sequence 23, Appl Sequence 35, Appl Sequence 35, Appl Sequence 35, Appl Sequence 31, Appl Sequence 32, Appl Sequence 34, Appl Sequence 36, Appl Sequence 37, Appl Sequence 38, Appl Sequence 38, Appl Sequence 39, Appl Sequence 39,
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Sequence 7, Apr
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                   Sequence
US-09-922-322-18
US-09-925-517A-13
US-09-825-517A-13
US-09-825-517A-13
US-10-602-141-9
US-10-604-401-22
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US-10-231-778-129
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        Sequence 11, Appl
Sequence 3, Appli
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Sequence 13, App
Sequence 13, App
Sequence 21, Appl
Sequence 21, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 4, Appli
Sequence 18, Appli
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                                                                                                                         May 4, 2004, 07:12:50 ; Search time 42 Seconds (without alignments) 65.998 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/NSC7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NBW_PUB.pep:*

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16: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO9_RW_PUB.pep:*

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13: /cgn2_6/ptodata/1/pubpaa/USO0_NBW_PUB.pep:*
                          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-925-322-11
US-09-825-517A-3
US-09-825-517A-10
US-10-046-922-33
US-10-094-401-133
US-10-96-403-21
US-10-462-262-101
US-09-777-908B-21
US-10-099-093-30
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US-10-151-204-21
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Listing first 250 summaries
                                                                                          - protein search, using sw model
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TOWNERTOWN: ALLIBEATURE

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FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (2).-(2)

OTHER INFORMATION: X2 is Asp, Gln, His, Ile, Leu, Lys, Met, Phe, or Thr;

NAME/KEY: MISC FEATURE

LOCATION: (3).-(3)

OTHER INFORMATION: X3 is His, Ile, Leu, Met, Phe, Pro, Trp, or Tyr;

NAME/KEY: MISC FEATURE

LOCATION: (4).-(4)

OTHER INFORMATION: X4 is Asp, His, Leu, or Ser (preferably Asp);

NAME/KEY: MISC FEATURE

LOCATION: (5).-(5)

OTHER INFORMATION: X Pro);

NAME/KEY: MISC FEATURE

LOCATION: (6).-(6)

OTHER INFORMATION: X Pro);

NAME/KEY: MISC FEATURE

LOCATION: (6).-(6)

OTHER INFORMATION: X is Ala, Arg, Asn, or Leu (preferably Leu);

LOCATION: (1).-(1)

OTHER INFORMATION: X is Ala, Arg, Asn, or Leu (preferably Leu);

LOCATION: (7).-(7)

OTHER INFORMATION: X is Ala, Arg, Asn, or Leu (preferably Leu);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dyax Corp.
APPLICANT: Dyax Corp.
APPLICANT: Dotter, James P.
APPLICANT: Delter, M. Daniel
APPLICANT: Delter, M. Daniel
APPLICANT: Delter, M. Daniel
APPLICANT: Ladner, M. Daniel
APPLICANT: Ladner, Robert Charles
TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (BLyS
TITLE OF INVENTION DAY-018.1 DCT. DYX-018.1 US
CURRENT APPLICATION NUMBER: US/09/932,322
CURRENT APPLICATION NUMBER: US/09/932,322
CURRENT APPLICATION NUMBER: 0501-08-17
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
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DOCATION: (7)...(7)
CTHER INFORMATION: X7 is 11e, Leu, Met, Pro, Ser, or Thr (preferably Thr);
NAME/KEY: MISC FEATURE
LOCATION: (8)..(8)
COTHER INFORMATION: X8 is Ala, Arg, Asn, Gly, His, Lys, Ser, or Tyr;
NAME/KEY: MISC FEATURE
LOCATION: (9)
COTHER INFORMATION: X9 is Ala, Arg, Asn, Gln, Leu, Met, Ser, Trp, Tyr, or Val;
US-09-932-613-11
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OTHER INFORMATION: X7 is 11e, Leu, Met, Pro, Ser, or Thr (preferably Thr);
NAME/KEY: MISC_FEATURE
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Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                100.0%; Score 26; DB 10; Length 10; 100.0%; Pred. No. 0.35; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/09932322
Publication No. US20030194743A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 10; Conservative
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OTHER INFORMATION: X5 is Ala, Arg, Asp, Glu, Leu, Phe, Pro, or Thr (preferably Glu
OTHER INFORMATION: r Pro);
NAME/KEY: MISC_FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: X6 is Ala, Arg, Asn, or Leu (preferably Leu);
NAME/KEY: MISC_FEATURE
NAME/KEY: MISC_FEATURE
                                                                        Sequence 8, Appli
Sequence 58, Appli
Sequence 78, Appli
Sequence 98, Appl
Sequence 63, Appl
Sequence 68, Appl
Sequence 103, Appl
Sequence 108, Appl
Sequence 108, Appl
Sequence 108, Appl
Sequence 108, Appl
Sequence 113, Appl
Sequence 114, Appl
Sequence 114, Appl
Sequence 114, Appl
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Sequence 33, Appli
Sequence 1, Appli
Sequence 247931,
Sequence 23, Appl
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NAME/KEY: MISC_FEATURE
LOCATION: (2).-(2)

OTHER INFORMATION: X2 is Asp, Gln, His, Ile, Leu, Lys, Met, Phe, or Thr;

NAME/KEY: MISC_FEATURE
LOCATION: (3).-(3)

OTHER INFORMATION: X3 is His, Ile, Leu, Met, Phe, Pro, Trp, or Tyr;

NAME/KEY: MISC_FEATURE
LOCATION: (4).-(4)

OTHER INFORMATION: X4 is Asp, His, Leu, or Ser (preferably Asp);

NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/09932613

Sequence 11, Application WG. 09303091565A1

GENERAL INFORMATION:

APPLICANT: Human Geneme Sciences, Inc.

APPLICANT: Beltzer, James P.

APPLICANT: Beltzer, Jones P.

APPLICANT: Beltzer, Tony J.

APPLICANT: Rosen, Craig A.

TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON

TITLE OF INVENTION: US/09/932,613

CURRENT APPLICANT: 2001-08-17

NUMBER OF SEQ ID NOS: 458

SOFTWARE: Patentin version 3.1

LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21,
Sequence 17,
                                                             Seguence 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-236-745-1
US-10-302-557-33
US-10-458-889-247931
US-10-011-859-23
US-10-113-273-14
US-10-153-273-17
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US-09-819-136-8
US-09-819-136-8
US-10-231-778-58
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US-10-231-778-68
US-10-231-778-103
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US-10-231-778-1108
US-10-231-778-103
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ORGANISM: Artificial Sequence
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APPLICANT: Rondon, Issac J
APPLICANT: Ladner, Robert C
TITLE OF INVENTION: BINDING PEPTIDES FOR CARCINOEMBRYONIC
TITLE OF INVENTION: ANTIGEN (CEA)
TITLE OF INVENTION: ANTIGEN (CEA)
TITLE REFERENCE: DYX.-016.1 (3421.1005-001)
CURRENT APPLICATION NUMBER: US/09/825,517A
CURRENT APPLICATION NUMBER: US/09/825,517A
PRIOR APPLICATION NUMBER: US/09/541,345
PRIOR PRING DATE: 2000-03
NUMBER OF SEQ ID NOS: 151
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 110
                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: VARIANT
LOCATION: 2
OTHER INFORMATION: X is Asn, Glu, Asp or Met
FEATURE:
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OTHER INFORMATION: X is Gln, Lys, Leu or Gly
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OTHER INFORMATION: X is Tyr, Trp or Ala
                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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GENERAL INFORMATION:
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NAME/KEY: VARIANT
LOCATION: 5
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                                                                                             Sequence 3, Application US/09825517A
| Sequence 3, Application US/09825517A
| Sequence 3, Application US/09825517A
| Publication No. US20030203415A1
| GENERAL INFORMATION:
| APPLICANT: Rondon, Issac J
| APPLICANT: BINDING PEPTIDES FOR CARCINOEMBRYONIC TITLE OF INVENTION: ANTIGEN (CEA)
| NUMBER OF SEQ ID NOS: 151
| SOFTWARE: FASICEO for Windows Version 4.0
| SEQ ID NOS: 151
| LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 26; DB 11; Length 10; 100.0%; Pred. No. 0.35; tive 0; Mismatches 0; Indels
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OTHER INFORMATION: Xaa is Asp, Gly, Ile, Lys, Phe or Thr
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US-09-825-517A-3
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LOCATION: 6
OTHER INFORMATION: Xaa is Arg, Asn, Asp, Glu or Gly
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LOCATION: 5
OTHER INFORMATION: Xaa is Ala, Gln, Gly, Lys or
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OTHER INFORMATION: Xaa is Asn, Leu, Met or Phe
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NAME/KEY: VARIANT
LOCATION: (8)...(8)
OTHER INFORMATION: Xaa is Ala, Trp or Tyr
FEATURE:
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LOCATION: (7)...(7)
OTHER INFORMATION: Xaa is Gln, Gly or Leu
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LOCATION: 2
OTHER INFORMATION: Xaa is Asn, Glu or Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE: OTHER INFORMATION: CEA binding loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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FEATURE:
NAME/KEY: VARIANT
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: X is Asn, Pro, Phe, Gly, Asp, Ala, Ser, Glu, Gln, OTHER INFORMATION: Trp, His, Arg, Met, Val or Leu
                                                                                                                                                                                                                                                                                                                                            Lys, Asn, Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: X is Lys, Phe, Asp, Gly, Leu, Asn, Trp, Ala, Gln
OTHER INFORMATION: or Thr
                                                                                                                                                                              NAME/KEY: VARIANT
LOCATION: 3
OTHER INFORMATION: X is Leu, Phe, Tyr, Trp, Val, Met, Ile or Asn
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Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 10; Conservative 0; Mismatches 0; Indels
FEATURE:
OTHER INFORMATION: Synthetic 16-mer microprotein analogue
                                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT
LOCATION: 4
OCHER INFORMATION: X is Phe, Leu, Asp, Glu, Ala, Ile,
OTHER INFORMATION: Val, Trp, Tyr, Gly or Thr
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US-10-046-922-33
Subjection US/10046922
Publication No. US20020164667A1
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Roivumen, Erkki
APPLICANT: Kubo, Hajime
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RESULT 4 US-09-825-517A-110 VS-09-825-517A-110 Publication No. US20030203415A1

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100.0%; Score 26; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 10; Conservative 0; Mismatches 0; Indels
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Sublication No. US20030207330A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sacot, Aaron K.
TITLE OF INVENTION: FIBRINGEN BINDING MOLETIES
FILE REFERENCE: DYX-036.1 DCT. DXX-036.1 US
CURRENT APPLICATION NUMBER: US/10/396,073
CURRENT FILING DATE: 2003-03-25
PRIOR FILING DATE: 2003-03-26
NUMBER OF SEQ ID NOS: 48
SEQ ILING DATE: 2002-03-26
SEQ ID NOS: 48
IENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: fibrinogen binding polypeptide
                                                                                                                                                                                    NAME/KEY: MISC FEATURE
LOCATION: (5)...(5)
OTHER INFORMATION: His, Met, Phe or Pro
NAME/KEY: MISC FEATURE
LOCATION: (6)...(6)
OTHER INFORMATION: Asn, Leu, or Thr
NAME/KEY: MISC FEATURE
LOCATION: (7)...(7)
OTHER INFORMATION: Arg, Asn, His, or Thr
NAME/KEY: MISC FEATURE
LOCATION: (8)...(8)
OTHER INFORMATION: Arg, Met, Phe, or Tyr
NAME/KEY: MISC FEATURE
LOCATION: (9)...(8)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (5). (5)
OTHER INFORMATION: X5 is Pro, Thr, or Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , COTHER INFORMATION: Asp, Gly, Phe, or Trp
US-10-094-401-133
Glu, Phe, or Met
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MISC_FEATURE
LOCATION: (3)...(3)
OCHER INFORMATION: X3 is Ala or Ser
FEATURE:
                                                                                                                                                               Ser, or Trp
                                                        LOCATION: (3)...(3)
OTHER INFORMATION: Asp, B
NAME/KEY: MISC FEATURE
LOCATION: (4)...(4)
OTHER INFORMATION: 11e, 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS-10-396-073-21
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NAME/KEY: SITE
LOCATION: (2)...(2)
OTHER INFORMATION: X is glycine or a conservative substitution
NAME/KEY: SITE
LOCATION: (3)...(4)
OTHER INFORMATION: X is tyrosine or a conservative substitution
NAME/KEY: SITE
LOCATION: (4)...(4)
OTHER INFORMATION: X is tryptophan or a conservative substitution
NAME/KEY: SITE
LOCATION: (5)...(5)
OTHER INFORMATION: X is leucine or a conservative substitution
NAME/KEY: SITE
LOCATION: (6)...(6)
OTHER INFORMATION: X is threonine or a conservative substitution
NAME/KEY: SITE
LOCATION: (6)...(6)
OTHER INFORMATION: X is threonine or a conservative substitution
NAME/KEY: SITE
LOCATION: (7)...(7)
OTHER INFORMATION: X is is isoleucine or a conservative substitution
NAME/KEY: SITE
LOCATION: (7)...(7)
OTHER INFORMATION: X is isoleucine or a conservative substitution
NAME/KEY: SITE
LOCATION: (7)...(7)
OTHER INFORMATION: X is isoleucine or a conservative substitution
NAME/KEY: SITE
LOCATION: (7)...(7)
OTHER INFORMATION: X is isoleucine or a conservative substitution
NAME/KEY: SITE
LOCATION: (7)...(7)
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COTHER INFORMATION: X is tryptophan or a conservative substitution
NAME/KEY: SITE
LOCATION: (9)...(9)
OTHER INFORMATION: X is glycine or a conservative substitution
US-10-046-922-33
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Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 10; Conservative 0; Mismatches 0; Indels
TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS FILE REFERENCE: 2896/737084A
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SEQ ID NO 33
LENGTH: ID
TYPE: PRI
ORGANISM: isolated peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sato, Aaron K.
APPLICANT: Sato, Aaron K.
APPLICANT: Sato, Arthur C.
APPLICANT: Ley, Arthur C.
APPLICANT: Ley, Arthur C.
APPLICANT: Cohen, Edward H.
TITLE OF INVENTION: SERUM ALBUMIN BINDING MOIETIES
FILE REFERENCE: DYX-026.2 PCT; DYX-026.2 US
CURRENT APPLICATION NUMBER: 60/331,352
PRIOR FILING DATE: 2001-03-09
PRIOR PILING DATE: 2001-03-09
PRIOR PILING DATE: 201-03-09
PRIOR PILING DATE: 201-05-23
NUMBER OF SEQ ID NOS: 271
SOFTWARE: PATENTING DATE: 201-05-23
NUMBER OF SEQ ID NOS: 271
LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 133, Application US/10094401 Publication No. US20030069395A1 GENERAL INFORMATION:
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1 LOCATION: (0) ...(0)
CTHER INFORMATION: Xaa is any amino acid residue except for cysteine US-09-757-908A-21
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Pred. No. 0.35;
; Mismatches 0; Indels
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Patent No. US20020052468A1

GENERAL INFORMATION: Darrell

TITLE OF INVENTION: Disulfide Core Polypeptides
FILE REFERENCE: 98-13D1

CURRENT FILING DATE: 2001-01-10

PRIOR FILING DATE: 1999-06-04

PRIOR PELING DATE: 1999-06-04

PRIOR FILING DATE: 1998-06-04

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 21

LENGTH: 14
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (9)...(0)
; OTHER INFORMATION: Xaa = Asp, Gly, Phe, or Trp
US-10-462-262-101
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Sequence 30, Application US/10098093
Sequence 30, Application US/10098093
Publication No. US20030092631A1
GENERAL INFORMATION:
APPLICANT: Debrayes, Kurt D.
APPLICANT: Lowman, Henry B.
APPLICANT: Schaffer, Michelle L.
APPLICANT: Schaffer, Michell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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OTHER INFORMATION: Sequence is synthesized
NAME/KEY: Xaa
                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 10; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 10, Conservative
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
US-09-757-908A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEATURE:
OTHER INFORMATION: example of serum albumin-binding agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (8)...(0)
OTHER INFORMATION: Xaa = Arg, Met, Phe, or Tyr
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OTHER INFORMATION: Xaa = Arg, Asn, His, or Thr
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FEATURE:
                                                                                                                                                           FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (8)...(8)
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (9)...(9)
LOCATION: (9)...(9)
LOCATION: (9)...(9)
US-10-396-073-21
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Publication No. US20040009534A1

GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
TITLE OF INVENTION: PROTEIN ANALYSIS
TITLE OF INVENTION: PROTEIN ANALYSIS
FILE REFERENCE: 10280-052001
CURRENT APPLICATION NUMBER: US/10/462,262
CURRENT FILING DATE: 2003-06-16
PRIOR PELICATION NUMBER: US 60/388,642
PRIOR PELICATION NUMBER: US 60/388,642
PRIOR FILING DATE: 2003-06-14
STOR FILING DATE: 2003-06-14
INUMBER OF SEQ ID NOS: 430
SOFTWARE: Fast-SEQ for Windows Version 4.0
ILENGTH: 10
TYPE: PRI
ORGANISM: Artificial Sequence
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      OTHER INFORMATION: X6 is ile, Met, or Tyr
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                                                              NAME/KEY: MISC_FEATURE LOCATION: (7)...(7) OTHER INFORMATION: X7 is Ala, His,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Xaa = Asp, Pro,
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LOCATION: 6
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NAME/KEY: VARIANT
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NAME/KEY: VARIANT
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LOCATION: 3
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LOCATION: (1)...(1)
OTHER INFORMATION: X1 is Asn, Asp, His, Leu, Phe, Pro, Ser, Tyr, or is absent (pr
OTHER INFORMATION: rably Ser);
NAME/KEY: MISC_FEATURE
LOCATION: (2)...(2)...(2)...(2)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3)...(3
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INFORMATION: X8 is Ala, Arg, Asp, Glu, Leu, Phe, Pro, or Thr (preferably Gl
INFORMATION: r Pro);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ser, or Thr (preferably Thr);
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; Sequence 4, Application US/09932613
; Sequence 4, Application US/09932613
; Publication No. US2000091565A1
; GADERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Fleming, Tony J.
APPLICANT: Fleming, Tony J.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: Dyx-025.1 US
CURRENT FILLING DATE: 2001-08-17
; CURRENT FILLING DATE: 2001-08-17
; CURRENT FILLING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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OTHER INFORMATION: X11 is Ala, Arg, Asn, Gly, His, Lys, Ser, or Tyr;
NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (5). (5)
OTHER INFORMATION: X5 is Asp, Gln, His, Ile, Leu, Lys, Met, Phe, or NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (6). (6) (6) or so is His, Ile, Leu, Met, Phe, Pro, Trp, or Tyr; NAME/KEY: MISC_FEATURE
LOCATION: (3)...(5)
CTHER INFORMATION: Each Xaa is independently any amino acid residue OTHER INFORMATION: except cysteine.
NAME/KEY: VARIANY
LOCATION: (4)...(14)
TICCATION: (4)...(14)
CTHER INFORMATION: Each Xaa is independently any amino acid residue
CTHER INFORMATION: except cysteine.
US-09-781-077-4
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NAME/KEY: MISC FEATURE
LOCATION: (8). (8)
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LOCATION: (9). (9) (9)
OTHER INFORMATION: X9 is Ala, Arg, Asn, or Leu (preferably Leu);
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                                                                                                                                                                                                                                                                                                                           100.0%; Score 26; DB 9; Length 15; 100.0%; Pred. No. 0.4;
                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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LOCATION: (10)...(10)
OTHER INFORMATION: X10 is 11e, Leu, Met, Pro,
NAME/KEX: MISC FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: BLyS binding polypeptide NAME/KEY: MISC FEATURE LOCATION: (1). [(1)
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Best Local Similarity 100.
Matches 10; Conservative
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LENGTH: 16
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                                                                                                                                                           Query Match 100.0%; Score 26; DB 14; Length 14; Best Local Similarity 100.0%; Pred. No. 0.39; Matches 10; Conservative 0; Mismatches 0; Indels
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Sequence 4, Application US/09781077

Sequence No. US20020012967A1

GENERAL INFORMATION:

APPLICANT: Holloway, James L.

APPLICANT: Jospers, Stephen R.

TITLE OF INVENTION: Insulin Homolog Polypeptide Zins4

FILE REFERENCE: 00-18

CURRENT APPLICATION NUMBER: US/09/781,077

CURRENT FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/188,544

PRIOR APPLICATION NUMBER: 60/188,544

PRIOR APPLICATION NUMBER: 60/188,544

PRIOR APPLICATION NUMBER: 60/188,544

SEQ ID NO 4

SEQ ID NO 4

LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-10-151-204-21
Sequence 21, Application US/10151204
Publication No. US20030148263A1
GENERAL INFORMATION:
APPLICANT: Larooca, David
APPLICANT: Baird, Andrew
APPLICANT: Baird, Andrew
APPLICANT: Baird, Andrew
TITLE OF INVENTION: GENETIC PACKAGE DISPLAY
FILE REPERBNCE: 760100.430G5
CURRENT APPLICATION NUMBER: US/10/151,204
CURRENT APPLICATION NUMBER: US/10/151,204
CURRENT APPLICATION NUMBER: US/10/151,204
SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 14
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LOCATION: 2, 3, 4, 5, 6, 7, 8, 9

COTHER INFORMATION: Xaa = Any Amino Acid
US-10-151-204-21
                      ; LOCATION: 1-2, 4-11, 13-14
; OTHER INFORMATION: Unknown amino acid
US-10-098-093-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: random peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: Motif
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXXXXXXXX 10
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RESULT 12

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Tue May

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APPLICANT: Ladner, Robert Charles
TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (BLy, FILLE REFERENCE: Dyx-018.1 US
FILLE REFERENCE: Dyx-018.1 US
CURRENT APPLICATION NUMBER: US/09/932,322
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: Patentin version 3.1
ESPQ ID NO 4
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: X15 is Asn, His, Leu, Pro, or Tyr (preferably His, Leu or Pro) NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or Thr (preferably G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: X3 is Asn, Asp, Leu, Pro, Ser, or Val (preferably Asn or Asp)
NAME/EVEY MISC (FRITURE
LOCATION: (5) 7 (7) 7 (8) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7 (9) 7
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INFORMATION: X2 is Arg, Asn, Asp, His, Phe, Ser, or Trp (preferably Arg);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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NAME/KEY: MISC_FEATURE
LOCATION: (1)...(1)
OTHER INFORMATION: X1 is Asn, Asp, His, Leu, Phe, Pro, Ser, Tyr, or is absent
OTHER INFORMATION: rably Ser);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: X16 is Asn, Asp, His, Phe, Ser, or Tyr, (preferably Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gly, Leu, Phe, Tyr, or Val (preferably Leu);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: X7 is Asp, His, Leu, or Ser (preferably Asp);
NAME/KEY: MISC FEATURE
LOCATION: (8). (8). (8)
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DUNCATION: (8)...(8)
OTHER INFORMATION: XP is Ala, Arg, Asp, Glu, Leu, Phe, Pro, OTHER INFORMATION: r Pro);
NAME/KEY: MISC_FEATURE
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OTHER INFORMATION: X14 is Asp,
NAME/KEY: MISC_FERTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10, Conservative
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US-09-932-322-18
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LOCATION: (12)...(12)
OTHER INFORMATION: X12 is Ala, Arg, Asn, Gln, Leu, Met, Ser, Trp, Tyr, or Val;
NAME/KEY: MISC TERATURE
LOCATION: (14)...(14)
OTHER INFORMATION: X14 is Asp, Gly, Leu, Phe, Tyr, or Val (preferably Leu);
NAME/KEY: MISC TERATURE
LOCATION: (15)...(15)
OTHER INFORMATION: X15 is Asn, His, Leu, Pro, or Tyr (preferably His, Leu or Pro);
NAME/KEY: MISC TERATURE
LOCATION: (16)...(16)
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FURDICATION NO. 1920030091565A1

FURDICATION NO. 1920030091565A1

FORDERAL INFORMATION:

APPLICANT: Human Genome Science, Inc.

APPLICANT: Potter, James P.

APPLICANT: Potter, M. Daniel

APPLICANT: Potter, M. Daniel

APPLICANT: Potter, M. Daniel

APPLICANT: Potter, James P.

APPLICANT: 
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OTHER INFORMATION: X is any amino acid except Cys NAME/KEY: MISC FEATURE
LOCATION: (5) ...(12)
OTHER INFORMATION: X is any amino acid except Cys NAME/KEY: MISC FEATURE
LOCATION: (14) ...(16)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09932322
Publication No. US20030194743A1
GENERAL INFORMATION:
APPLICANT: Dyax Corp.
APPLICANT: Beltzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Peter, M. Daniel
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US-09-932-322-4
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APPLICANT: Ladner, Robert C
1TILE OF INVENTION: BINDING PEPTIDES FOR CARCINOEMBRYONIC
1TILE OF INVENTION: ANTIGEN (CEA)
1TILE OF INVENTION NUMBER: US /09/825,517A
1TILE OF ILL OF ANTIGEN (CEA)
1STOR FILING DATE: 2000-04-03
1NUMBER OF SEQ ID NOS: 151
1NUMBER OF SEQ ID NOS: 151
1NUMBER OF SEQ IO Windows Version 4.0
1SEQ ID NO 13
1LENGTH: 16
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Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: VARIANT
LOCATION: (12)...(12)
OTHER INFORMATION: Kaa is Ala, Gly, His, Phe, Thr or Val
                                                                                                                                                                                                                                                                                                                                     LOCATION: (7)...(7)
OTHER INFORMATION: Xaa is Asp, Gly, Ile, Lys, Phe or Thr
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LOCATION: (14)...(14)
OTHER INFORMATION: Xaa is Asn, Gln, Phe, Ser or Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: VARIANT
LOCATION: (9)...(9)
OTHER INFORMATION: Xaa is Arg, Asn, Asp, Glu or Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (8)...(8)
OTHER INFORMATION: Xaa is Ala, Gln, Gly, Lys or Thr
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; CTHER INFORMATION: Xaa is Leu, Ser, Trp or Tyr
US-09-825-517A-1
                                                                                                                                                                                                                                    LOCATION: 6
JTHER INFORMATION: Xaa is Asn, Leu, Met or Phe
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OTHER INFORMATION: Xaa is Ala, Trp or Tyr
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LOCATION: (10)...(10)
OTHER INFORMATION: Xaa is Gln, Leu or Gly
                                                                                                                                                         THER INFORMATION: Xaa is Asn, Glu or Met
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ORGANISM: Artificial Sequence
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NAME/KEY: VARIANT
LOCATION: (16)...
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US-09-825-517A-13
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APPLICANT: Beltzer, James P.
APPLICANT: Beltzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
TITE OF INVENTOR: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (BLyS)
FILE REFERENCE: Dyx-018.1 PCT; DXx-018.1 US
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 16
TYPE
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APPLICANT: Rondon, ISSAC J
APPLICANT: Ladner, Robert C
TITLE OF INVENTION: BINDING PEPTIDES FOR CARCINOEMBRYONIC; TITLE OF INVENTION: ANTIGEN (CEA); FILE REPERENCE: DYX-016.1 (3421.1005-001); FILE REPERENCE: DYX-016.1 (3421.1005-001); FILE REPERENCE: 2003-324; PRIOR APPLICATION NUMBER: US/09/825,517A; PRIOR APPLICATION NUMBER: US 09/541,345; PRIOR FILING DATE: 2000-04-03; NUMBER OF SEQ ID NOS: 151; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: phage display library template NAME/KEY: MISC_FEATURE LOCATION: (1)...(3) COTHER INFORMATION: X is any amino acid except Cys NAME/KEY: MISC_FEATURE LOCATION: (5)...(12) COTHER INFORMATION: X is any amino acid except Cys NAME/KEY: MISC_FEATURE LOCATION: (14)...(16)
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NAME/KEY: VARIANT
LOCATION: 1
OTHER INFORMATION: Xaa is Asn, Asp or is absent
FEATURE:
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OTHER INFORMATION: CEA binding polypeptide
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OTHER INFORMATION: Xaa is Trp
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                    LOCATION: (1)...(16)
OTHER INFORMATION: amino acid positions 4 and 13 are invariant Cys;
OTHER INFORMATION: all other positions Xaa are varied but not Cys, to
OTHER INFORMATION: provide a library of 2.5x10(8) different peptides
OTHER INFORMATION: based on the template sequence
FEATURE:
OTHER INFORMATION: Parental domain for design of microprotein display
OTHER INFORMATION: library
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OTHER INFORMATION: X is Phe, Leu, Asp, Glu, Ala, Ile, Lys, ASn, Ser,
OTHER INFORMATION: Val, Trp, Tyr, Gly or Thr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 26; DB 11; Length 16; Best Local Similarity 100.0%; Pred. No. 0.4; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WESULA 1-517A-111
Sequence 111, Application US/09825517A
Sequence 111, Application US/09825517A
Sequence 111, Application US/09825517A
Sequence 111, Application US/09825517A
SERVERAL INFORMATION:
APPLICANT: Rondon, Issac J
APPLICANT: Ladner, Robert C
TITLE OF INVENTION: BINDING PEPTIDES FOR CARCINOEMBRYONIC
TITLE OF INVENTION: ANTIGEN (CEA)
FILE REFERENCE: DYX-016.1 (341.1005-001)
CURRENT APPLICATION NUMBER: US/09/825,517A
CURRENT APPLICATION NUMBER: US 09/541,345
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 151
SOFTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION: X is Val, Ile, Met, Tyr, Phe, Pro or Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Synthetic 16-mer microprotein analogue
                                                                                                                                                                                                                                                                                 ; FEATURE:

NAME/KEY: VARIANT

LOCATION: 1, 2, 3, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16

OTHER INFORMATION: Xaa = Any Amino Acid except Cys
US-09-825-517A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1
OTHER INFORMATION: X is Asp, Asn, Ala or Ile
FEATURE:
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OTHER INFORMATION: X is Asn, Glu, Asp or Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 2
OTHER INFORMATION: X is Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CXXXXXXX 10
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LOCATION: 3
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                                                                                                                  NAME/KEY: VARIANT
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Gaps
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OTHER INFORMATION: X is Phe, Thr, Met, Ser, Ala, Asn, Val, His, 1le,
OTHER INFORMATION: Pro, Trp, Tyr, Gly, Leu or Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: VARIANT
LOCATION: (15)...(15)
OTHER INFORMATION: X is Val, Leu, Ile, Pro, Ala, Gln, Ser, Met, Glu,
OTHER INFORMATION: Thr, Lys, Trp or Arg
                     LOCATION: (8)...(8)
OTHER INFORMATION: X is Lys, Phe, Asp, Gly, Leu, Asn, Trp, Ala, Gln,
OTHER INFORMATION: Y Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (16)...(16)
OTHER INFORMATION: X is Leu, Met, Val, Tyr, Ala, Ile, Trp, His, Pro, OTHER INFORMATION: Gln, Glu, Phe, Lys, Arg or Ser
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| Publication No. US20040071705A1
| Publication No. US20040071705A1
| GENERAL INFORMATION
| APPLICANT: Sato, Aarch K. | APPLICANT: Sato, Abert TITLE OF INVENTION: LIGANDS AND IDENTIFICATION METHOD THEREFOR FILE REPRENCE: 10280-058001
| TITLE OF INVENTION: LIGANDS AND IDENTIFICATION METHOD THEREFOR FILE REPRENCE: 10280-058001
| CURRENT APPLICATION NUMBER: US 60/390,657 | PRIOR FILING DATE: 2002-06-21 | NUMBER OF SEQ. ID NOS: 11 | SOFTWARE: FastSEQ for Windows Version 4.0 | SEQ. ID NO 9 | LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (14)...(14)
OTHER INFORMATION: X is Asn, Asp, Glu, Pro, Gln, Ser, Phe, or Val
                                                                                                                                                           LOCATION: (9)...(9)
OTHER INFORMATION: X is Asn, Pro, Phe, Gly, Asp, Ala, Ser, Glu, OTHER INFORMATION: Trp, His, Arg, Met, Val, or Leu
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OTHER INFORMATION: Xaa = any amino acid except cysteine (Cys)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 26; DB 11; Length 16; Best Local Similarity 100.0%; Pred. No. 0.4; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                        LOCATION: (10)...(10)
OTHER INFORMATION: X is Gln, Lys, Leu or Gly
                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (11)...(11)
OTHER INFORMATION: X is Trp, Tyr or Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
OTHER INFORMATION: template sequence
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ORGANISM: Artificial Sequence
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NAME/KEY: VARIANT
                                                                                                                                   NAME/KEY: VARIANT LOCATION: (9)...(9
                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: VARIANT
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NAME/KEY: VARIANT
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NAME/KEY: VARIANT
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TITLE OF INVENTION: SERUM ALBUMIN BINDING MOIETIES
FILE REFERENCE: DYX-026.2 PCT; DYX-026.2 US
CURRENT APPLICATION NUMBER: US/10/094,401
CURRENT FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: 60/331,352
PRIOR PLIING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEC ID NOS: 271
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1)...(1)
OTHER INFORMATION: ATC, Phe, or Tyr
NAME/FEY: MISC_FEATURE
LOCATION: (2)...(2)
OTHER INFORMATION: ATC, Leu, Ser, or Trp
NAME/FEY: MISC_FEATURE
LOCATION: (3)...(3)
OTHER INFORMATION: ASC, ASP, Phe, or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCATION: (10)...(10)
OTHER INFORMATION: Arg, Asn, His, or Thr
NAME/REY INFORMATION: Arg, Met, Phe, or Thr
OTHER INFORMATION: Arg, Met, Phe, or Tyr
NAME/REY INFORMATION: Asg, Gly, Phe, or Tyr
OTHER INFORMATION: Asp, Gly, Phe, or Trp
NAME/REY INFORMATION: Asp, Gly, Phe, or Trp
OTHER INFORMATION: Asp, Gly, Phe, or Trp
NAME/REY INFORMATION: Ala, Asn, or Asp
NAME/REY INFORMATION: Ala, Asn, or Asp
OTHER INFORMATION: Ala, Ash, or Asp
OTHER INFORMATION: Arg, Phe, Pro, or Tyr
IOCATION: (15)...(15)
OTHER INFORMATION: Arg, Phe, Pro, or Tyr
IOCATION: (16)...(16)
                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE: OTHER INFORMATION: albumin binding peptide
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COTHER INFORMATION: Arg, His, Phe, or Ser US-10-094-401-134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: MISC FEATURE
LOCATION: (5)...(5)
OTHER INFORMATION: Gln, Glu, Phe, or Met
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; Sequence 238, Application US/10094401
; Publication No. US20030069395A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (6). (6)
OTHER INFORMATION: ASP, Pro, or Thr
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NAME/KEY: MISC FEATURE
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                                                                                                                                                                                                                                                                                       SEQ ID NO 134
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 10, Conservative
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LOCATION: (9). (9)
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OTHER INFORMATION: Asp, Phe, His, Leu, Asn, Pro, Arg, Ser, Trp, and Tyr
NAME/KEY: MISC FEATURE
COCHION: (3)...(3)

OTHER INFORMATION: Ala, Asp, Glu, Phe, Gly, His, Leu, Asn, Pro, Arg, Ser, Val, Trp,
OTHER INFORMATION: and Tyr
NAME/KEY: MISC FEATURE
LOCATION: (5)...(12)
OTHER INFORMATION: any amino acid except Cys
NAME/KEY: MISC FEATURE
LOCATION: (1)...(12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Ala, Asp, Glu, Phe, Gly, His, Leu, Asn, Pro, Arg, Ser, Val, Trp, OTHER INFORMATION: and Tyr
NAME/KEY: MISC_FEATURE
LOCATION: (15):.(16)
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US-10-094-401-22
                                                                                                                       0; Gaps
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                                                       Query Match
100.0%; Score 26; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels
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OTHER INFORMATION: variegated display library template
NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                          Sequence 22. Application US/10094401
FUNDICATION OF US20030069395A1
GENERAL INFORMATION:
APPLICANT: SAto, Aaron K.
APPLICANT: Cohe, Behard H.
TITLE OF INVENTION: SERUM ALBUMIN BINDING MOIETIES
FILE REFERENCE: DYX-026.2 PC7. DYX-026.2 US
CURRENT APPLICATION NUMBER: US/10/094,401
PRIOR FILING DATE: 2002-03-08
PRIOR FILING DATE: 2001-03-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 22
US-10-094-401-134
US-10-094-401-134
; Sequence 134, Application US/10094401
; Publication No. US20030069395A1
; GENERAL INFORMATION:
; APPLICANT: DAX CORP.
; APPLICANT: Bato, Aaron K.
; APPLICANT: Cohen, Edward H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                        1 CXXXXXXX 10
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      US-10-602-141-9
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LENGTH: 16
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Sequence 157, Application US/10158825

Sequence 157, Application US/10158825

Publication No. US2003013894A1

GENERAL INFORMATION:

APPLICATY: Tom Parry et al.

TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity

FILE REFERENCE: PF555

CURRENT APPLICATION NUMBER: 60/294,976

PRIOR APPLICATION NUMBER: 60/294,976

PRIOR APPLICATION NUMBER: 60/294,976

NUMBER OF SEQ ID NOS: 158

SOFTWARE: PatentIn version 3.1

LENGTH: 16

TYPE: REPERTOR OF 158
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100.0%; Score 26; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                             100.0%; Score 26; DB 14; Length 16; 100.0%; Pred. No. 0.4; tive 0; Mismatches 0; Indels
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Publication No. US20030199671A1

GENERAL INFORMATION:
APPLICANT: Rond. Isaac Jesus
APPLICANT: Buy, Arthur C.
APPLICANT: Ransohoff, Thomas C.
APPLICANT: Ransohoff, Thomas C.
APPLICANT: Potter, M. Daniel (decesed)
TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION
TITLE OF INVENTION: POLYPETIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MISC FEATURE LOCATION: (1)...(3)
OTHER INFORMATION: X equals any amino acid
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LOCATION: (5)...(12)
OTHER INFORMATION: X equals any amino acid
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; OTHER INFORMATION: X equals any amino acid US-10-158-825-157
                                            FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (14) ... (16)
OTHER INFORMATION: X equals any amino acid
US-10-158-847-157
LOCATION: (5)..(12)
OTHER INFORMATION: X equals any amino acid
                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 26
US-10-125-869A-12
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 25
US-10-158-825-157
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COTHER INFORMATION: Ala, Asp, Phe, Gly, His, Leu, Asn, Pro, Gln, Arg, Ser, Val, Trp, OTHER INFORMATION: Or Tyr
NAME/KEY: MISC_FEATURE
LOCATION: (15)...(16)
COTHER INFORMATION: Asp, Phe, His, Leu, Asn, Pro, Arg, Ser, Trp, or Tyr
US-10-094-401-238
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Publication No. US20030091557A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Tom Patry et al.

TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
FILIS REFRENCE: PREST

CURRENT APPLICATION NUMBER: US/10/158,847

CURRENT FILING DATE: 2002-06-03

PRIOR FILING DATE: 2001-06-04

NUMBER OF SEQ ID NOS: 158

SOFTWARE: Patentin version 3.1

INNOTH: 16

INNOTH: 16
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100.0%; Score 26; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                 APPLICANT: Sato, Aaron K.
APPLICANT: Ley, Arthur C.
APPLICANT: Ley, Arthur C.
APPLICANT: Ley, Arthur C.
TITLE OF INVENTION: SERUM ALBUMIN BINDING MOIETIES
FILE REFERENCE: DYX-026.2 PCT; DYX-026.2 US
CURRENT APPLICATION NUMBER: US/10/094,401
CURRENT FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: 60/331,352
PRIOR APPLICATION NUMBER: 60/331,352
PRIOR PILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/232,975
PRIOR PILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 271
SQCTWARE: Patentin version 3.1
SEQ ID NO 28
LENGTH: 16
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OTHER INFORMATION: X equals any amino acid
FEATURE:
NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXXXXXXXX 10
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ORGANISM: homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
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US-10-158-847-157
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                                                                                                                                                                                                                                                                                                                         LOCATION: 1, 2, 3, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16 OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: VARIANT
LOCATION: 1, 2, 3, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16
OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: 1, 2, 3, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16; corner information: xaa = Any Amino Acid US-10-125-869A-12
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OTHER INFORMATION: X3 is Leu or Tyr, preferably Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 27
US-10-396-073-20

US-10-396-073-20

Sequence 20, Application US/10396073

Publication No. US20030207330A1

GENERAL INFORMATION:

APPLICANT: Wescort, Charles R.

TILE OF INVENTION: FIBRINOGEN BINDING MOIETIES

TILE REFERENCE: DYX-036.1 US

CURRENT APPLICATION NUMBER: US/10/396,073

CURRENT FILING DATE: 2003-03-25

PRIOR APPLICATION NUMBER: US 60/367,645

PRIOR APPLICATION NUMBER: US 60/367,645

PRIOR APPLICATION NUMBER: US 60/367,645

NUMBER OF SEQ ID NOS: 48

SEQ ID NOS: 48

SEQ ID NOS: 48

SEQ ID NOS: 40

LENGTH: 16
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LOCATION: (1)._(1)
OTHER INFORMATION: X1 is His, Leu, or Phe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOCATION: (S):.(S)
OTHER INFORMATION: X5 is Asn, Met, or Ser
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CURRENT FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: 60/284,534
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 200
SOFTWARE: FastSEQ for Windows Version 4.0
ESCY ID NO 12
LENGTH: 16
                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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NAME/KEY: MISC_FEATURE
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ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: VARIANT
LOCATION: 1, 2, 3
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION: X12 is Trp or Tyr, preferably Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Sato, Aaron K.
TITLE OF INVENTION: FIRENINGEN BINDING MOIETIES
FILE REFERENCE: DXX-036.1 PCT. DXX-036.1 US
CURRENT APPLICATION NUMBER: US/10/396,073
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: US 60/367,645
PRIOR PELLING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 48
SEQ ID NOS: 48
SEQ ID NO 31
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: X16 is Asn, Phe, or Ser US-10-396-073-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (14)...(14)
OTHER INFORMATION: X14 is Asn, His, or Val
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: X15 is Asp, Phe, or Pro
                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (10)..(10)
OTHER INFORMATION: X10 is Ala, His, or Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (11)...(11)
OTHER INFORMATION: X11 is Leu, Pro, or Tyr
                                                                                     LOCATION: (7)...(7)
OTHER INFORMATION: X7 is Arg, Asn, or Tyr
                                                                                                                                                                                           LOCATION: (8/...(8)
OTHER INFORMATION: X8 is Pro, Thr, or Trp
                                                                                                                                                                                                                                                                                LOCATION: (9).7(9)
OTHER INFORMATION: X9 is Ile, Met, or Tyr
LOCATION: (6)..(6)
OTHER INFORMATION: X6 is Ala or Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Sequence 31, Application US/10396073 , Publication No. US20030207330A1 , GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wescott, Charles R.
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NAME/KEY: MISC_FEATURE
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NAME/KEY: MISC FEATURE
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                                                                    NAME/KEY: MISC_FEATURE
                                                                                                                                                            NAME/KEY: MISC FEATURE
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US-10-396-073-31
                                                                                                                                                                                   LOCATION:
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S, W, or

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L, N, P,

OTHER INFORMATION: X1 and X2 are D, F, H,

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TYPE: PRT
ORGANISM: Artificial Sequence
ORGANISM:
PEATURE:
OTHER 'INFORMATION: example of serum albumin-binding agents
PEATURE:
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NAME/KEY:
VARIANT
(10)...(0)
OTHER INFORMATION: Xaa = Arg, Asn, His, or Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 2
DIHER INFORMATION: Xaa = Arg, Leu, Ser, or Trp
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THER INFORMATION: Xaa = Gln, Glu, Phe, or Met
BATURE:
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THER INFORMATION: Xaa = Asn, Asp, Phe, or Tyr
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OCATION: (8)...(0)
THER INFORMATION: Xaa = His, Met, Phe or Pro
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THER INFORMATION: Xaa = Arg, Met, Phe or Tyr
RESULT 30
US-10-462-262-102
Squence 102, Application US/10462262
Publication No. US20040009534A1
GENERAL INFORMATION:
APPLICANT: Barc, Aaron K.
TITLE OF INVENTION: PROTEIN ANALYSIS
FILE REFERENCE: 10280-025001
CURRENT APPLICATION WOMBER: US/10/462,262
CURRENT APPLICATION NUMBER: US 60/388,642
PRIOR APPLICATION NUMBER: US 60/388,642
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
SRIGHEN OF SEQ ID NOS: 430
SOFTWARE: FRAESEQ FOR WINGOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: VARIANT
LOCATION: (14)...(0)
OTHER INFORMATION: Xaa = Ala, Asn, or Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAMI/KEY: VARIANT
LOCATION: 1
OTHER INFORMATION: Xaa = Arg, Phe, or Tyr
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DTHER INFORMATION: Xaa = Asp, Gly, Phe,
FEATURE:
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LOCATION: (9)...(0)
JTHER INFORMATION: Xaa = Asn, Leu,
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THER INFORMATION: Xaa = Asp, Pro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: VARIANT
JOCATION: (7)...(0)
JTHER INFORMATION: Xaa = 11e, Ser,
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IAME/KEY: VARIANT
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                                                                                                                                          LOCATION: (5). [12)
OTHER INFORMATION: X5, X6, X7, X8, X9, X10, X11 and X12 are any amino acid except
OTHER INFORMATION: Cys
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; OTHER INFORMATION: Xaa = any common alfa-amino acids, except cysteine
US-10-462-262-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 3. 14

COTHER INFORMATION: Xaa = Ala, Asp, Glu, Phe, Gly, His, Leu, Asn, Pro, OTHER INFORMATION: Arg, Ser, Val, Trp, and Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: VARIANT
LOCATION: 1, 2, 15, 16
OTHER INFORMATION: Xaa = Asp, Phe, His, Leu, Asn, Pro, Arg, Ser, Trp,
OTHER INFORMATION: and Tyz
                                                                                                                                                                                                                                                                        or
                                                                                                                                                                                                                                                                                                        NAME/KEY: MISC FEATURE
LOCATION: (15)...(16)
COTHER INFORMATION: X15 and X16 are D, F, H, L, N, P, R, S, W, or Y US-10-396-073-31
                                                                               or
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100.0%; Score 26; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels
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Publication No. US20040009534A1
GENERAL INFORMATION
GENERAL INFORMATION
TILE APPLICANT: SATO, ABTON K.
TILE ROFINENTION: PROTEIN AMALYSIS
TILE REFERENCE: 10280-052001
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: US 60/388,642
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 430
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 16
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OTHER INFORMATION: template sequence
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                                                                                                                                                                                                                      MAME/KEY: MISC_FEATURE
LOCATION: (14)...(14)
OTHER INFORMATION: X14 is A, D, F,
                                                                               О,
F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
                  FEATURE:
NAMBÉKEY: MISC FEATURE
COCATION: (3)...(3)
OTHER INFORMATION: X3 is A,
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CXXXXXXXX 10
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                                                                                                                       NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: VARIANT
LOCATION: 3, 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: VARIANT
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RESULT 29 US-10-462-262-22

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FEATURE:

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Sequence 35, Application US/09938315

Sequence 35, Application US/09938315

Parent No. US2020091085A1

GENERAL INFORMATION:
THORN, TANTEN R.
THORN, JUDITH M.
QUILLIAM, LAWRENCE A.
DER, CHANNING J.
ITILE OF INVENTION: Src SH3 BINDING PEPTIDES AND METHODS OF
ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                       amino acid sequence of TN10/V library
                                                                                                                                                                                                                                                                                                                                                                                                                                                             or v
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MISC_FEATURE
LOCATION: (1) .. (12)
CUTHER INFORMATION: X is A,E,G,L,P,Q,R, or V
NAME/KEY: MISC_FEATURE
LOCATION: (10) .. (10)
CUTHER INFORMATION: X is F,I,K,L,M,N or Y
NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,315
FILING DATE: 23-Aug-2001
CLASSIFICATION: «Unknown»
                                                          NAME/KEY: MISC_FEATURE

COTER INFORMATION: X

OTHER INFORMATION: X

NAME/KEY: MISC_FEATURE

COTTION: (9): (9)

OTHER INFORMATION: X

NAME/KEY: MISC_FEATURE

OTHER INFORMATION: X

NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                      LOCATION: (16)...(16)
OTHER INFORMATION: X is D.F.H,I,L,N,V or Y
NAME/KEY: MISC_FRATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: X is I,K,M,N,R,S, or T
US-09-957-607-45
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NAME: Villacorta, Gilberto M.
REGISTRATION NUMBER: 34,038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (14) (14)
OTHER INFORMATION: X is A,D,G,H,L,P,R,
NAME/FEY: MISC.EATURE
COCATION: (8) (8) (8) (9) (7)
OTHER INFORMATION: X is A,E,G,L,P,Q,R,
                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (7)...(7)
OTHER INPORMATION: X is A,D,G,H,L,P,R,
NAME/KEY: MISC, FRATURE
(A)
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CXXXXXXX 10
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US-09-938-315-35
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| Sequence 45, Application US/09957607
| Sequence 45, Application US/09957607
| Sequence No. US20020076728A1
| GENERAL INFORMATION:
| APPLICANT: Macleman, John M. APPLICANT: Ladner, Robert C. | TITLE OF INVENTION: Engineering Affinity Ligands for Macromolecules | TILE REFERENCE: DYX-001.1 US-1 | CURRENT PAPLICATION NUMBER: US/09-19 | PRIOR APPLICATION NUMBER: 08/821,498 | PRIOR APPLICATION NUMBER: 08/81,498 | PRIOR APPLICATION WUMBER: 08/819,885 | PRIOR FILING DATE: 1996-03-20 | PRIOR FI
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATANAN MAMBIXES: VARIANT LOCATION: (0)...(0) OTHER INFORMATION: Xaa is any amino acid residue except for cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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100.0%; Score 26; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels
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100.0%; Score 26; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATE: CONKIIN, Darrell
TITLE OF INVENTION: Disulfide Core Polypeptides
FILE REFERENCE: 98-1301
CURRENT APPLICATION NUMBER: US/09/757,908A
CURRENT FILING DATE: 2001-01-10
PRIOR FILING DATE: 1999-06-04
PRIOR FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: US 60/088,136
PRIOR FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 17
LOCATION: (15)...(0)
OTHER INFORMATION: Xaa = Arg, Phe, Pro, or Tyr
                                                                                                                                   ) LOCATION: (16)...(0)

, OTHER INFORMATION: Xaa = Arg, His, Phe, or Ser

US-10-462-262-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19, Application US/09757908A Patent No. US20020052468A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin version 3.1
SEQ ID NO 45
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 CXXXXXXXX 17
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CXXXXXXX 10
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                                                                         FEATURE:
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-757-908A-19
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Sequence 63, Application US/098589358
; Sequence 65, Application US/098589358
; Publication No. US20030069177A1
; GENERAL INFORMATION:
APPLICANT: Dubaquie, Yves
APPLICANT: Filvaroff, Ellen
TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
FILE REFERENCE: P1794R1
CURRENT APPLICATION NUMBER: US/09/858,9358
; CURRENT FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: US 60/248,985
PRIOR APPLICATION NUMBER: US 60/204,490
PRIOR PILING DATE: 2000-05-16
; WIMBER OF SEQ ID NOS: 153
; SEQ ID NO 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 26; DB 14; Length 19; 100.0%; Pred. No. 0.42; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
FITLE OF INVENTION: ISOLATING AND USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: OTHER INFORMATION: Sequence is synthesized
                 CORRESPONDENCES: 467
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORREST: 1155 Avenue of the Americas
CITY: New York
CITY: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISP C COMPACTION
                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 16-FEB-1966
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Lessie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (612) 869-9741/8864
TELEFAX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Xaa
LOCATION: 1-5, 7-14, 16-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 10; Conservative
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US-09-858-935B-63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 80, Application US/10046922
; Sequence 80, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; TITLE OF INYENTION: VEGER-3 INHIBITOR MATERIALS AND METHODS
; TILE REFERENCE: 2896/37084A
; CURRENT FALLIGATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; SOFTWARE: Patentin version 3.0
; SEQ ID NOS: 80
; SEQ ID NOS: 80
; SEQ ID NOS: 80
; SED ID NOS: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 26; DB 13; Length 19; Best Local Similarity 100.0%; Pred. No. 0.42; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 26; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 10; Conservative 0; Mismatches 0; Indels
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    REFERENCE/DOCKET NUMBER: 4980-007-0 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                     ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FRAGMENT TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-938-315-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , LOCATION: (11)..(18)
; OTHER INFORMATION: X is any amino acid US-10-046-922-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: SITE LOCATION: (2)..(8) OTHER INFORMATION: X is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SPARKS, Andrew B.
APPLICANT: TAN, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: PER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James TITLE OF INVENT
                                               TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 35, Application US/10161791
Publication No. US20030186863A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CXXXXXXXX 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: peptide
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Gaps

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Query Match
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: MISC FEATURE
LOCATION: (10) (10)
OTHER INFORMATION: His, Met, Phe or Pro
NAME/KEY: MISC FEATURE
LOCATION: (11) (11)
OTHER INFORMATION: Asn, Leu, or Thr
NAME/KEY: MISC FEATURE
LOCATION: (12) (12)
OTHER INFORMATION: Arg, Msn, His, or Thr
NAME/KEY: MISC FEATURE
LOCATION: (13) (13)
OTHER INFORMATION: Arg, Met, Phe, or Tyr
NAME/KEY: MISC FEATURE
LOCATION: (14) (14)
OTHER INFORMATION: Asp, Gly, Phe, or Trp
NAME/KEY: MISC FEATURE
LOCATION: (16) (16)
OTHER INFORMATION: Asp, Gly, Phe, or Trp
NAME/KEY: MISC FEATURE
LOCATION: (16) (16)
OTHER INFORMATION: Ala, Asn, or Asp
NAME/KEY: MISC FEATURE
LOCATION: (15) (16)
OTHER INFORMATION: Ala, Phe, Pro, or Tyr
NAME/KEY: MISC FEATURE
LOCATION: (17) (18)
                                                         OTHER INFORMATION: albumin binding peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (18) ... (18); OTHER INFORMATION: Arg, His, Phe, or Ser US-10-094-401-135
                                                                                                                                                                                                                                                                                                                Met
                                                                                                                                                                                                                                                                                                                Glu, Phe, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                or Trp
                                                                                                                                                                                                                                                                                                                                                                              or Thr
                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                       COCATION: (8)...(8)
OTHER INFORMATION: ASP, Pro,
NAME/KEY: MISC_FEATURE
LOCATION: (9)...(9)
OTHER INFORMATION: 11e, Ser,
                                                                                                                                                                LOCATION: (4) ...(4)
OTHER INFORMATION: AFG, LA
NAME/KEY: MISC_FEATURE
LOCATION: (5)...(5)
OTHER INFORMATION: ABN, ABN
NAME/KEY: MISC_FEATURE
LOCATION: (7)...(7)
OTHER INFORMATION: G1n, G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CXXXXXXXX 15
                                                                             NAME/KEY: MISC FEATURE LOCATION: (3)...(3) OTHER INFORMATION: Arg, NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MISC FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 39
US-10-098-093-23
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                                                                                                           Gaps
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                                                                                                                                                                                                                                                US-10-271-869-63
US-10-271-869-63
Sequence 63, Application US/10271869
Sequence 63, Application No. US2003211992A1
Sequence 67, Application No. US2003211992A1
SENDICAMY: Dubaqqile, Yves
APPLICAMY: Dubaqqile, Yves
APPLICAMY: Lowman, Henry B.
TILLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
FILE REPERBNCE: P1794R1
CURRENT APPLICATION NUMBER: US/10/271,869
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: US/09/858,935
PRIOR FILING DATE: 2002-07-02
PRIOR PILING DATE: 2000-11-15
PRIOR FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 63
LENGTH: 20
                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                             Query Match 100.0%; Score 26; DB 10; Length 20; Best Local Similarity 100.0%; Pred. No. 0.43; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: STACO, ABTON K.
APPLICANT: SATO, ABTON K.
APPLICANT: Cacho, ABTON K.
APPLICANT: Cacho, Edward H.
TITLE OF INTENTION: SERUM ALBUMIN BINDING MOIETIES
FILE REFERENCE: DYX-026.2 PCT; DYX-026.2 US
CURRENT APPLICATION NUMBER: 08/10/094,401
CURRENT PLING DATE: 2002-03-08
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR PLILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 271
SOFTWARE: Parentin version 3.1
SEQ ID NO 135
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: Sequence is synthesized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Xaa
LOCATION: 1-5, 7-14, 16-20
CTHER INFORMATION: Unknown amino acid
US-10-271-869-63
, OTHER INFORMATION: Unknown amino acid US-09-858-935B-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 135, Application US/10094401
Publication No. US20030069395A1
GENERAL INFORMATION:
APPLICANT: DYAX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CXXXXXXXC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CXXXXXXXX 15
                                                                                                                                                       1 CXXXXXXXC 10
                                                                                                                                                                                                6 CXXXXXXXX 15
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Gaps

0; Gaps

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Query Match 100.0%; Score 26; DB 15; Length 20; Best Local Similarity 100.0%; Pred. No. 0.43; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
OTHER INFORMATION: example of serum albumin-binding agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 7
OTHER INFORMATION: Xaa = Gln, Glu, Phe, or Met FRATURE:
NAME/KEY: VARIANT
LOCATION: 8
OTHER INFORMATION: Xaa = Asp, Pro, or Thr
FRATURE:
NAME/KEY: VARIANT
LOCATION: (9)...(0)
OTHER INFORMATION: Xaa = 11e, Ser, or Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: VARIANT
LOCATION: (13)...(0)
OTHER INFORMATION: Xaa = Arg, Met, Phe, or Tyr
FEATURE:
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: VARIANT
LOCATION: 5
LOCATION: 5
FEATURE: INFORMATION: Xaa = Asn, Asp, Phe, or Tyr
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: VARIANT
LOCATION: (10) ... (0)
OTHER INFORMATION: Xaa = His, Met, Phe or Pro
                                                                                                                                                                                                                                                                           Sequence 103, Application US/10462262; Sequence 103, Application US/10462262; Publication No. US2004000534A1
GENERAL INFORMATION; APPLICANT: Sato, Aaron K.
APPLICANT: Sato, Aaron K.
APPLICANT: Bawson, Bruce M.
TITLE OF INVENTION: PROTEIN ANALYSIS
FILE REFERENCE: 10280-05201
CURRENT APPLICATION NUMBER: US/10/462,262
CURRENT FILING DATE: 2003-06-16
PRIOR PRILIGATION NUMBER: US 60/388,642
PRIOR PRILIGATION DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 430
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: VARIANT
LOCATION: (12)...(0)
OTHER INFORMATION: Xaa = Arg, Asn, His, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (11)...(0)
OTHER INFORMATION: Xaa = Asn, Leu, or Thr
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 3
OTHER INFORMATION: Xaa = Arg, Phe, 03
FEATURE:
NAME/KEY: VARIANT
LOCATION: 4
COTER INFORMATION: Xaa = Arg, Leu, Se
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                 1 CXXXXXXXX 10
                                                                                                                             1 CXXXXXXXC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: VARIANT
                                                                                                                                                                                                                                                    RESULT 41
US-10-462-262-103
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OTHER INFORMATION: Description of Artificial Sequence: Illustrative
OTHER INFORMATION: zinc finger peptide
                                                                                                                                                                                                                                                                                                                            .
0
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; SEQ ID NO 23

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INCORDATION: Sequence is synthesized

; IOCATTON: 1-5, 7-14, 16-20

; CTHER INCORDATION: Unknown amino acid

US-10-098-093-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: HILO, YORU
APPLICANT: NAGAI, KENICHI
APPLICANT: NAGAI, KENICHI
APPLICANT: TRIE, RYOTARO
APPLICANT: TRIE, RYOTARO
APPLICANT: TARE, RYOTARO
APPLICANT: TOSHIKAN, TSUTOMU
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: NAGHARI, KENJI
APPLICANT: NAGHARI: SAGIIO
CURRENT APPLICATION NUMBER: 105/10/094,749
CURRENT APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PALCHING DATE: 2010-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PALCHING DATE: 2010-09-14
NUMBER OF SEQ ID NOS: 3381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (17)...(19)
; CTHER INFORMATION: Variable amino acid
US-10-094-749-3381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (11)..(15)
OTHER INFORMATION: Variable amino acid
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LOCATION: (2)...(9)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 40
US-10-094-749-3381
Sequence 3381, Application US/10094749
Publication No. US20030219741A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ISOGAL, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: SHIL, SHIZUKO
APPLICANT: YAMMOTO, JUN-ICHI
APPLICANT: ISONO, YUKKO
APPLICANT: HIO, YUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                     1 CXXXXXXX 10
                                                                                                                                                                                                                                                                                                                                                                                                                6 CXXXXXXXX 15
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LOCATION: (11)..(
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Gaps

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Indels

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Best Local Similarity 100.0%; Pred. No. 0.45; Matches 10; Conservative 0; Mismatches
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100.0%; Score 26; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 60601

COMPUTER READABLE FORM:

MEDIUUT TYPE: Floppy disk
COMPUTER: 1EM PC compatible
COMPUTER: 1EM PC compatible
COMPUTER: 1EM PC compatible
COMPUTER: PATCHIN: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/969,192
PILING DATE: 01-Oct-2001
APPLICATION NUMBER: US 9-455061
FILING DATE: 06-DEC-1999
APPLICATION NUMBER: US 9-130225
APPLICATION NUMBER: US 9-130225
FILING DATE: 21-AUG-1998
APPLICATION NUMBER: US 9-701124
FILING DATE: 21-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT. 4.
US-09-969-192-5
US-09-969-192-5
; Sequence 5, Application US/09969192
; Patent No. US20020151027A1
; GENERAL INFORMATICAN:
APPLICANT: WICKIAM, THOMAS J.
ROELVINK, PETRUS W.
KOVESDI, INRE
; TITLE OF INVENTION: TRAGETING ADENOVIRUS WITH USE OF
CONSTRAINED PEPTIDE MOTIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STATE: 1111nois
COUNTRY: USA
     LOCATION: (14)...(0)
OTHER INFORMATION: Xaa = Asp, Gly, Phe, or Trp
FEATURE:
                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: VARIANT
LOCATION: (18)...(0)
COTATION: (28)...(0)
US-10-462-262-103
                                                                                                                                                                           NAME/KEY: VARIANT
LOCATION: (17)...(0)
OTHER INFORMATION: Xaa = Arg, Phe, Pro, or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Hefner, M. Daniel
REGISTRATION NUMBER: 41,826
REFERENCE/DOCKET NUMBER: 213564
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                       NAME/KEY: VARIANT
LOCATION: (16)...(0)
OTHER INFORMATION: Xaa = Ala, Asn, or Asp
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: Linear

NOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-969-192-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXXXXXXXX 10
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100.0%; Score 26; DB 9; Length 23;

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APPLICANT: Rudolph-Owen, Laura A. APPLICANT: Rudolph-Owen, Laura A. APPLICANT: Rudolph-Owen, Laura A. APPLICANT: Curtis, Rory A.J.
APPLICANT: Curtis, Rory A.J.
APPLICANT: Galvin, Katherine M. APPLICANT: Galvin, Katherine M. APPLICANT: Galvin, Miyoung C. APPLICANT: Silos-Santiago, Immaculada APPLICANT: Silos-Santiago, Immaculada APPLICANT: Silos-Santiago, Immaculada APPLICANT: Millianden, Mark J. APPLICANTON NUMBER: US 10/225, 13967, Millianden, Mark APPLICANTON NUMBER: US 60/205, 447
PRIOR FILING DATE: 2000-11-09
PRIOR PILING DATE: 2000-11-13
PRIOR PILING DATE: 2000-11-14
PRIOR PILING DATE: 2000-11-15
PRIOR PELING DATE: 2000-11-15
PRIOR PILING DATE: 2000-02-18
PRIOR PILING DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 119
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 119
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Millennium Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEATURE:
OTHER INFORMATION: Consensus sequence FEATURE:
NAME/KEY: VARIANT
LOCATION: (2) ... (9)
OTHER INFORMATION: Xaa = Any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: VARIANT
LOCATION: (11)...(16)
OTHER INFORMATION: Xaa = Any amino acid
                                                                                                                                                                                                                                                                              Application US/10423543
o. US20040058355A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Libermann, Rosana K.
Hunter, John J.
Meyers, Rachel E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
1 CXXXXXXX 10
                                                                          1 CXXXXXXXX 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: VARIANT
LOCATION: (18)...(20)
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RESULT 45
US-10-161-791-36
Sequence 36, Application US/10161791
Sequence 36, Application US/10161791
Publication No. US20030186863A1
GENERAL INFORMATION:
APPLICANT: SPRKS, Andrew B. APPLICANT: GULLIAM, Lawrence A. APPLICANT: QUILLIAM, Lawrence A. APPLICANT: PER, Channing J. APPLICANT: FOWLKES, Dana M. APPLICANT: RIDER, James B. IITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF TILLE OF INVENTION: ISOLATING AND USING SAME NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEDE: Pennie & PACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 26; DB 14; Length 28; Best Local Similarity 100.0%; Pred. No. 0.47; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/09919603
Patent No. US20020137679A1
GENERAL INCOMPATION:
APPLICANT: LAWIET, John W.
TITLE OF INVENTION: COMP/TSP-1, COMP/TSP-2 and Other TSP
FILE REFERENCE: 1440.1033-007
CURRENT APPLICATION NUMBER: US/09/919,603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATION SYSTEM: PC-COMPATION SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTOWNEY/ABENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEGISTRATION NUMBER: 18,872
REPERNOE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAX: (212) 869-9741/8864
TELEX. (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXXXXXXXX 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KAY, BRIAN K.
SPARKS, ANDREW B.
THORN, JUDITH M.
QUILLIAM, LAWRENCE A.
DER, CHANNING J.
TITLE OF INVENTION: Src SH3 BINDING PEPTIDES AND METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENČE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MCDUON ILER: FLORY WILLS

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/938,315

FILING DATE: 23-Aug-2001

CLASSIFICATION: AUMNOMN-

ATTORNEY/AGENT INFORMATION:

NAME: Villacorta, Gilberto M.

RECISTRATION NUMBER: 34,038

REFERENCE/DOCKET WUMBER: 4980-007-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 26; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 10; Conservative 0; Mismatches 0; Indels
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 36:

; LOCATION: (1)...(25)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-423-543-119

                                                                              NAME/KEY: VARIANT LOCATION: (22)...(24)
OOTHER INFORMATION: Xaa = Any amino acid FRATURE:
                                   OTHER INFORMATION: Xaa = Any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 36, Application US/09938315
Patent No. US20020091085A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CXXXXXXXX 10
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                                                                                                                                                                   NAME/KEY: VARIANT
LOCATION: (1)...(
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Gaps

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RESULT 48

US-10-231-778-116

US-10-231-778-116

US-10-231-778-116

PUBLICATION NO. US20030126647A1

FORMATION:

APPLICANT: BILOGEAU, Plerre

APPLICANT: Chaudhury, Abdul M.

APPLICANT: Chaudhury, Abdul M.

APPLICANT: Chaudhury, Abdul M.

APPLICANT: BILOGEAU, Ming and M.G.

APPLICANT: BOLOGEAU, Ming and M.G.

APPLICANT: Beacock, William J.

TITLE OF INVENTION: Method for inducing seed development by down-regulating TITLE OF INVENTION: Method for inducing seed development by down-regulating TITLE OF INVENTION: Method for inducing seed development by down-regulating APPLICANT: 129-94

TITLE OF INVENTION: Method for inducing seed development by down-regulating TITLE OF INVENTION: Method for inducing seed development by down-regulating APPLICATION NUMBER: US/10/231,778

CURRENT APPLICATION NUMBER: US/10/231,778

FRIOR FILING DATE: 1999-09-20

PRIOR PELLOR DATE: 1998-09-22

PRIOR FILING DATE: 1998-09-22

PRIOR FILING DATE: 1998-09-22

PRIOR FILING DATE: 1998-09-22

PRIOR FILING DATE: 1998-07-01

PRIOR PLING DATE: 1999-07-01

PRIOR PLING DATE: 1999-07-01
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                                                                                                                      Query Match 100.0%; Score 26; DB 14; Length 35; Best Local Similarity 100.0%; Pred. No. 0.51; Matches 10; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: VARIANT; LOCATION: (1)...(35); LOCATION: (1)...(35)
OTHER INFORMATION: X at positions 1 to 35 is any amino acid.
US-10-231-778-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 26; DB 14; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 199, Application US/10289660; Publication No. US20030157561A1; GENERAL INFORMATION: APPLICANT: KOLKWAN, JOOST A. APPLICANT: STEWMER, WILLEM P.C. APPLICANT: GOVINDARAJAN, SRIDHAR
; OTHER INFORMATION: Any amino acid US-10-133-128-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CXXXXXXXC 10
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US-10-289-660-199
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publication No. US20030082630A1
General Information:
FILE PETERBNCE:
GURRENT FILING DATE:
GURRENT FILING DATE:
GO12-04-26
FRIOR PELICATION NUMBER: G0/374,107
FRIOR FILING DATE: 2002-04-18
FRIOR FILING DATE: 2001-11-26
FRIOR FILING DATE: 2001-11-26
FRIOR FILING DATE: 2001-11-26
FRIOR FILING DATE: 2001-11-19
FRIOR FILING DATE: 2001-11-14-26
FRIOR FILING DATE: 2011-14-26
FRIOR FILING DATE: 2011-14-26
FRIOR FILING DATE: 2011-14-26
FRIOR FILING DATE: 2011-13-15
FRIOR FILING DATE: 2011-13-15
FRIOR FILING DATE: 2011-14-26
FRIOR FILING DATE: 2011-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    o
O
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CCATION: 6, 7, 8, 9, 10, 11, 13, 14, 15, 16, 17, 18, 19, 20

CTHER INFORMATION: Xaa = Any Amino Acid

US-09-919-603-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 26; DB 9; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 10; Conservative 0; Mismatches 0; Indels
; CURRENT FILING DATE: 2001-07-30; PRIOR APPLICATION NUMBER: PCT/US00/02482; PRIOR FILING DATE: 2000-02-01; PRIOR FILING DATE: 1999-02-01; PRIOR FILING DATE: 1999-02-01; NUMBER: OF SEQ ID NOS: 21; SOFTWARE: PastSEQ for Windows Version 4.0; SEQ ID NO 13 LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MOD RES
LOCATION: (2)...(7)
OTHER INFORMATION: Any amino acid
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MORABS KEY: MOL RES
LOCATION: (9) ... (12)
OTHER INFORMATION: Any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (14)..(19)
OTHER INFORMATION: Any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (21\overline{1})..(25)
OTHER INFORMATION: Any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MOD_RES
LOCATION: (14)..(1
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LOCATION: (21) (
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US-10-133-128-199
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NS-10-204-145-5
Sequence 5, Application US/10204145
Publication No US20040023291A1
Publication No US20040023291A1
GENERAL INFORMATION:
APPLICANT: Ecole Pelytechnique Federale de Lausanne
APPLICANT: Spertini, Francois
ITILE OF INVENTION: NOVEL BES VENOM POLYPEPTIDES AND METHODS OF USE THEREOF
ITILE REFERENCE: 18519-00-10-064 20349-543
CURRENT APPLICATION NUMBER: US/10/204,145
CURRENT FILING DATE: 2002-08-16
PRIOR PELICATION NUMBER: US.S.N. 09/506,978
NUMBER OF SEQ ID NOS: 5
SEQ ID NOS: 5
LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-903-248-1
Sequence 1, Application US/09903248
Sequence 1, Application US/09903248
Patent No. US20020102263A1
Fatent No. US20020102263A1
FAPRICANT: Wands, Jack R.
APPLICANT: de la Monte, Suzanne M.
APPLICANT: Ince, Nedim
APPLICANT: Larlson, Rolf I.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
FILE REPRENCE: 21486-032 DIVS
CURRENT APPLICATION NUMBER: US/09/903,248
CURRENT PILING DATE: 2001-07-11
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1
LENGTH: 36
                                                                                                                                                                                                  Gaps
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ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORWATION: Description of Artificial Sequence: Consensus
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OTHER INFORMATION: Description of Artificial Sequence: CYSTEINE OTHER INFORMATION: SPACING MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 26; DB 16; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                             Query Match
100.0%; Score 26; DB 14; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FEATURE:
; OTHER INFORMATION: Where any X can be any amino acid.
US-10-204-145-5
                                                  ; FEATURE:
; OTHER INFORMATION: Where any X can be any amino acid.
US-10-174-151-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-174-151-5

Sequence 5, Application US/10174151

Sequence 10 No. US20030165514A1

SEDICANT: Spertini, Francois

TITLE OF INVENTION: NOVEL BEE VENOM POLYPEPTIDES AND METHODS OF USE THEREOF

TITLE REFERENCE: 18519-001

CURRENT PAPLICATION NUMBER: US/10/174,151

CURRENT FILING DATE: 2002-06-18

PRIOR FILING DATE: 2000-02-18

NUMBER OF SEQ ID NOS: 5

SEQ ID NO 5

LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT

OKGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
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     TITLE OF INVENTION: COMBINATORIAL LIBRARIES OF MONOMER DOMAINS FILE REPERENCE: 0319.510US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 26; DB 14; Length 35; Best Local Similarity 100.0%; Pred. No. 0.51; Matches 10; Conservative 0; Mismatches 0; Indels
                                  FILE REFERENCE: 0319-510US
CURRENT APPLICATION NUMBER: US/10/289,660
CURRENT FILING DATE: 2003-11-06
PRIOR APPLICATION NUMBER: 10/133,128
PRIOR FILING DATE: 2002-04-26
PRIOR PELLOR DATE: 2002-04-36
PRIOR PELLOR DATE: 2002-04-18
PRIOR FILING DATE: 2001-11-26
PRIOR FILING DATE: 2001-11-26
PRIOR FILING DATE: 2001-11-19
PRIOR PLING DATE: 2001-11-19
PRIOR PLING DATE: 2001-04-26
NUMBER: OF SEQ ID NOS: 244
SEQ ID NO 199
LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MOD_RES; LOCATION: (27)...(34)
COTHER INFORMATION: Any amino acid
US-10-289-660-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: MOD RES
LOCATION: (14)..(19)
OTHER INFORMATION: Any amino acid
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OTHER INFORMATION: Any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (2)...(7)
OTHER INFORMATION: Any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (9)...(12)
OTHER INFORMATION: Any amino acid
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ORGANISM: Artificial Sequence
PEATURE:
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NAME/KEY: MOD RES
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NAME/KEY: MOD_RES
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LOCATION: (21)..(
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27 CXXXXXXX 36
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LENGTH: 36
TYPE: PRT
                                                                                 RESULT 54
US-09-903-063-1
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Patent No. US20020110559A1

GENERAL INFORMATION:

APPLICANT: Wands, Jack R.

APPLICANT: Wands, Jack R.

APPLICANT: Deluch, Alan H.

APPLICANT: Deluch, Hosein A.

TITLE OF INVENTION INGRES: 21486-032 CIP

CURRENT APPLICATION NUMBER: US/09/859,604

CURRENT APPLICATION NUMBER: US/09/859,604

CURRENT FILING DATE: 1209-11-08

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1

LENGTH: 36

TYPE: RT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Consensus
OTHER INFORMATION: EGF-like domain
NAME/KEY: VARIANT
OTHER INFORMATION: Wherein any Xaa may be any amino acid
NAME/KEY: VARIANT
OTHER INFORMATION:
NAME/KEY: VARIANT
OTHER INFORMATION: Wherein Xaa is any amino acid
NAME/KEY: VARIANT
NAME/KEY: VARIANT
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
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Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 26; DB 9; Length 36; 100.0%; Pred. No. 0.51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
            NAME/KEY: VARIANT
LOCATION: (2)..(8)
OTHER INFORMATION: Wherein Xaa is any amino acid
NAME/KEY: VARIANT
LOCATION: (10)..(13)
OTHER INFORMATION: Wherein Xaa is any amino acid.
NAME/KEY: VARIANT
LOCATION: (15)..(24)
OTHER INFORMATION: Wherein Xaa is any amino acid.
NAME/KEY: VARIANT
LOCATION: (26)
OTHER INFORMATION: Wherein Xaa is any amino acid.
NAME/KEY: VARIANT
LOCATION: (26)
OTHER INFORMATION: Wherein Xaa is any amino acid.
NAME/KEY: VARIANT
LOCATION: (28)..(35)
OTHER INFORMATION: Wherein Xaa is any amino acid.
US-09-903-248-1
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CTHER INFORMATION: Wherein Xaa is any amino acid.
NAME/KEY: VARIANT
LOCATION: (28)..(35)
OTHER INFORMATION: Wherein Xaa is any amino acid.
US-09-859-604-1
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OTHER INFORMATION: Wherein Xaa is anu amino acid.
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
OTHER INFORMATION: EGF-like domain
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Best Local Similarity 100.
Matches 10; Conservative
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US-09-859-604-1
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JOHERALI IN CANCENTION:
APPLICANT: Wands, Jack R.
APPLICANT: Wands, Jack R.
APPLICANT: Wands, Jack R.
APPLICANT: Ge la Monte, Suzanne M.
APPLICANT: Ince, Nedim
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
FILE REPERROR: 21486-032 DIV2
CURRENT APPLICATION NUMBER: US/09/903,216
CURRENT APPLICATION NUMBER: US/09/903,216
CURRENT APPLICATION NUMBER: 09/436,184
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1
LENGTH: 36
Sequence 1, Application US/09903063

Sequence 1, Application US/09903063

Batent No. US20020114810A1

GENERAL INFORMATION:

APPLICANT: Wands, Jack R.

APPLICANT: Ince Nedim

APPLICANT: Ince Nedim

APPLICANT: Ince Nedim

APPLICANT: Ince Nedim

APPLICANT: OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS

TILE REFERENCE: 21486-032 DIV3

CURRENT FILING DATE: 2001-10-11

PRIOR FILING DATE: 1999-11-08

NUMBER OF SEQ ID NOS: 9

SOFTWARE PATENTIN VEY: 2.1
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OTHER INFORMATION: Description of Artificial Sequence: Consensus
OTHER INFORMATION: EGF-like domain
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100.0%; Score 26; DB 9; Length 36;
Best Local Similarity .100.0%; Pred. No. 0.51;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: VARIANT
| LOCATION: (2). (8)
| OTHER INFORMATION: Wherein Xaa is any amino acid
| OTHER INFORMATION: Wherein Xaa is any amino acid
| NAME/KEY: VARIANT
| LOCATION: (13)
| OTHER INFORMATION: Wherein Xaa is any amino acid.
| NAME/KEY: VARIANT
| LOCATION: (12)
| OTHER INFORMATION: Wherein Xaa is any amino acid.
| NAME/KEY: VARIANT
| LOCATION: (24)
| OTHER INFORMATION: Wherein Xaa is any amino acid.
| NAME/KEY: VARIANT
| LOCATION: (28)
| OTHER INFORMATION: Wherein Xaa is any amino acid.
| NAME/KEY: VARIANT
| LOCATION: (28)
| OTHER INFORMATION: Wherein Xaa is any amino acid.
| US-09-903-063-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09903216 Patent No. US20020114811A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CXXXXXXXX 10
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Sequence 1, Application US/0903023
; Sequence 1, Application US/0903023
; Patent No. US20020146421A1
; GADERAL INFORMATION:
APPLICANT: Wands, Jack R.
APPLICANT: Galson, Rolf I.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
CURRENT APPLICATION NUMBER: 032 DIV1
CURRENT FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: 09/436,184
PRIOR APPLICATION NUMBER: 09/436,184
PRIOR SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
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LENGTH: 36

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: EGF-like domain
NAME/KEY: VARIANT
LOCATION: (2) .. (8)
OTHER INFORMATION: Wherein Xaa is any amino acid
NAME/KEY: VARIANT
LOCATION: (10) .. (13)
OTHER INFORMATION: Wherein Xaa is any amino acid
NAME/KEY: VARIANT
LOCATION: (10) .. (13)
OTHER INFORMATION: Wherein Xaa is any amino acid.
NAME/KEY: VARIANT
LOCATION: (2) .. (24)
OTHER INFORMATION: Wherein Xaa is any amino acid.
NAME/KEY: VARIANT
LOCATION: (26) .. (35)
OTHER INFORMATION: Wherein Xaa is any amino acid.
NAME/KEY: VARIANT
COTHER INFORMATION: Wherein Xaa is any amino acid.
NAME/KEY: VARIANT
COTHER INFORMATION: Wherein Xaa is any amino acid.
US-09-903-023-1
                          Gaps
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APPLICANT: Wands, Jack R.
APPLICANT: de la Monte, Suzanne M.
APPLICANT: Ince, Nedim
APPLICANT: Carlson, Rolf I.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
FILE REPERENCE: R.I. Hosp. - Malignant Neoplasms
CURRENT APPLICATION NUMBER: US/09/436,184
CURRENT FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VET. 2.0
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100.0%; Score 26; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 10; Conservative 0; Mismatches 0; Indels
                       Indels
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0
100.0%; Pred. No. 0.51;
                          0; Mismatches
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Publication No. US20030031670A1
GENERAL INFORMATION:
APPLICANT: Wends, Jack R.
APPLICANT: de la Monte, Suzanne M.
Best Local Similarity 100.
Matches 10; Conservative
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US-09-436-184-1
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US-09-903-023-1
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                                                           OTHER INFORMATION: Description of Artificial Sequence: Consensus OTHER INFORMATION: EGF-like domain OTHER INFORMATION: (2)...(8)

NAMMYKEY: VARIANT
LOCATION: (2)...(8)

OTHER INFORMATION: Wherein Xaa is any amino acid
LOCATION: (10)...(13)

OTHER INFORMATION: Wherein Xaa is any amino acid.
LOCATION: (10)...(24)

OTHER INFORMATION: Wherein Xaa is any amino acid.
LOCATION: (15)...(24)

OTHER INFORMATION: Wherein Xaa is any amino acid.

NAMME/KEY: VARIANT
LOCATION: (26)...(26)
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LOCATION: (2)..(8)
OTHER INFORMATION: Wherein Xaa is any amino acid NAME/KEY: VARIANT
LOCATION: (10)..(13)
OTHER INFORMATION: Wherein Xaa is any amino acid.
NAME/KEY: VARIANT
LOCATION: (10)..(13)
OTHER INFORMATION: Wherein Xaa is any amino acid.
LOCATION: (15)..(24)
LOCATION: (15)..(24)
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LOCATION: (26)
OTHER INFORMATION: Wherein Xaa is any amino acid.
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LOCATION: (28)..(35)
OTHER INFORMATION: Wherein Xaa is any amino acid.
                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Wherein Xaa is any amino acid.
NAME/KEY: VARIANT
LOCATION: (28)..(35)
                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (28)..(35)
OTHER INFORMATION: Wherein Xaa is any amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: Biologau, Pierre
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Dennis, Elizabeth S.
APPLICANT: Dennis, Elizabeth S.
APPLICANT: Dennis, Elizabeth S.
APPLICANT: Luo, Ming
APPLICANT: Luo, Ming
APPLICANT: Luo, Ming
APPLICANT: Dennis, Elizabeth S.
APPLICANT: Luo, Ming
APPLICANT: Dennis, Elizabeth S.
APPLICANT: Dennis, AU PP6661
APPLICANT: Dennis, AU PP6662
APPLICANT: Dennis, AU PP6663
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      Gaps
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Best Local Similarity 100.0%; Score 26; DB 14; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 10; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: VARIANT; LOCATION: (1)..(36); OTHER INFORMATION: X at positions 1 to 36 is any amino acid. US-10-231-778-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 120, Application US/10231778
Publication No. US20030126647A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-231-778-120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/10138158
Publication No. US20030036509A1
GENERAL INFORMATION:
APPLICANT: STER CELL PHARMACEUTICALS, INC.
APPLICANT: TWARDZIK, Daniel R.
APPLICANT: PELKER, Thomas S.
APPLICANT: PELKER, Thomas S.
APPLICANT: PELKER, Thomas S.
APPLICANT: PERKEL, Stefan
APPLICANT: RENO, John M.
TITLE OF INVENTION: TGF-alpha POLYPEPTIDES, FUNCTIONAL FRAGMENTS AND METHODS OF USE CURRENT APPLICATION NUMBER: US/10/138,158
CURRENT FILING DATE: 2002-08-08
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                                                                                                                                                                                                                                                                                                                                               Gaps
; SEQ ID NO 1

LENGTH: 36

CREANISM: Artificial Sequence
COTHER INFORMATION: Description of Artificial Sequence: Consensus
COTHER INFORMATION: EGF-like domain
COTHER INFORMATION: Wherein any Xaa may be any amino acid
US-09-436-184-1
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                                                                                                                                                                                                                                                                                  100.0%; Score 26; DB 10; Length 36; 100.0%; Pred. No. 0.51; tive 0; Mismatches 0; Indels
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100.0%; Score 26; DB 14;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 10; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2002-08-08
PRIOR APPLICATION WUMBER: US 09/641,587
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 2000-04-26
PRIOR FILING DATE: 1099-12-13
PRIOR APPLICATION NUMBER: US 09/459,813
PRIOR FILING DATE: 1999-12-13
PRIOR APPLICATION NUMBER: US 09/492,935
PRIOR FILING DATE: 1999-12-13
PRIOR FILING DATE: 1999-18-19
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MISC_FEATURE
1 LOCATION: (1)...(36)
2 OTHER INFORMATION: Xaa is any amino acid
10S-10-138-158-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bilodeu, Pierre
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Dennis, Elizabeth S.
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 10; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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US-10-231-778-117
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US-10-231-778-118

Sequence 118, Application US/10231778

Publication No. US20030126647A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bilodeau, Pierre
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Anna M.G.
APPLICANT: Luo, Ming Hilama M.G.
APPLICANT: Luo, Ming William J.G.
APPLICANT: Beacock, William J.G.
APPLICANT: Boomis, Elizabeth S.
APPLICANT: William J.G.
APPLICANT: NUMBER: US/10/231,778

CURRENT APPLICATION NUMBER: GO/101,184

PRIOR FILING DATE: 1998-09-21
PRIOR APPLICATION NUMBER: AU PP6061
PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: AU PP6063
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1990-07-01
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Publication No. US20030126647A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ghaudhury, Abdul M.
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Luo, Min M.G.
APPLICANT: Dennis, Elizabeth S.
APPLICANT: Dennis, Elizabeth S.
APPLICANT: APPLICANT: Anna M.G.
APPLICANT: Peacock, William J.
TITLE OF INVENTION: Method for inducing seed development by down-regulating TILE OF INVENTION: expression of the FIS2 gene
TITLE OF INVENTION: WENDERS: US/10/231,778

CURRENT APPLICATION NUMBER: US/10/231,778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Motif
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Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 10; Conservative 0; Mismatches 0; Indels
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: LOCATION: (1)..(37)

: OTHER INFORMATION: X at positions 1 to 37 is any amino acid.

US-10-231-778-118
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ORGANISM: Artificial Sequence
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1 CXXXXXXXX 10
                                                                    CXXXXXXXXC 28
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US-10-231-778-118
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Sequence 124, Application US/10231778

Publication No. US20030126647A1

GENERAL INVOCANTION

HapelCANT: Chaudhury, Abdul M.

APPLICANT: Luo, Ming

APPLICANT: Luo, Ming

APPLICANT: Luo, Ming

APPLICANT: Peacock, William J.

APPLICANTON NUMBER: US/10/231,778

CURRENT FILING DATE: 1998-09-22

PRIOR PILING DATE: 1998-09-22

PRIOR PILING DATE: 1998-09-22

PRIOR FILING DATE: 1998-07-01

PRIOR FILING DATE: 1998-07-01

PRIOR FILING DATE: 1998-07-01

PRIOR FILING DATE: 1998-07-01

PRIOR FILING DATE: 1999-07-01

PRIOR PRIOR PRIOR DATE: 1999-07-01
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PRIOR APPLICATION NUMBER: AU PQ1346
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ 1D NOS: 239
SOFTWARE: Patentin Ver. 2.0
SEQ 1D NO 120
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
FEATURE:
FEATURE:
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CCATTON: (1)..(36)

OTHER INFORMATION: X at positions 1 to 36 is any amino acid.
US-10-231.~778-124
                                                                                                                                                                                                                                                                                                                                                                                                        , NAME/KEY: VARIANT

, LOCATION: (1)..(36)

, OTHER INFORMATION: X at positions 1 to 36 is any amino acid.

US-10-231-778-120
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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Gaps

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RESULT 66
US-10-231-778-131
Sequence 11. Application US/10231778
Publication No US20030126647A1
Sequence 11. Application VG US20030126647A1
Sequence 11. Application No US20030126647A1
Sequence 11. Application No US20030126647A1
APPLICANT: Chaudhury, Abdull M. APPLICANT: Chaudhury, Abdull M. G. APPLICANT: Rolling, Mill M. G. Mill M. G. APPLICANT: Duo, Wing M. G. Mill M. G. M
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Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 10; Conservative 0; Mismatches 0; Indels
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LOCATION: (1)..(37)
COTHER INFORMATION: X at positions 1 to 37 is any amino acid. US-10-231-778-131
                                                         FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Motif
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)..(37)
COTHER INFORMATION: X at positions 1 to 37 is any amino acid.
US-10-231-778-125
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 10; Conservative 0; Mismatches 0; Indels
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              ORGANISM: Artificial Sequence
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US-10-386-055-41
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APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Duo, Ming
APPLICANT: Luo, Ming
APPLICANT: Luo, Ming
APPLICANT: Peacock, William J.
APPLICANT: Peacock, William J.
APPLICANT: Beacock, William J.
APPLICANT: Duo, Ming
APPLICANTON: expression of the FIS2 gene
TITLE OF INVENTION: expression of the FIS2 gene
TITLE OF INVENTION: Wethod for inducing seed development by down-regulating
TITLE OF INVENTION: WINBER: US/10/231,778
CURRENT APPLICATION NUMBER: 05/102,184
PRIOR PILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1999-07-01
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OTHER INFORMATION: Description of Artificial Sequence: Motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)..(37)
COTHER INFORMATION: X at positions 1 to 37 is any amino acid.
US-10-231-778-121
CURRENT FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: 09/398,237
PRIOR FILING DATE: 1999-09-09-09
PRIOR FILING DATE: 1999-09-20
PRIOR PLING DATE: 1998-09-21
PRIOR PLING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: AU PP6061
PRIOR PELING DATE: 1998-09-22
PRIOR PELING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: AU PP6063
PRIOR PILING DATE: 1998-09-22
PRIOR PILING DATE: 1998-09-22
PRIOR PILING DATE: 1999-07-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
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APPLICANT: Bllodeau, Pierre
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Columbw, Anna M.G.
APPLICANT: Koltumow, Anna M.G.
APPLICANT: Peacock, William J.
APPLICANT: Peacock, William J.
TITLE OF INVENTION: Method for inducing seed development by down-regulating FILE REFRENCE: 72-98A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: VARIANT
LOCATION: 2,6-19,21-27,29,31-34,36
OTHER INFORMATION: The Xaa amino acid residue at these positions can be
OTHER INFORMATION: any amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or 4 can
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OTHER INFORMATION: or Tyr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The amino acid residue at position 30 can be Asp
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OTHER INFORMATION: The number of residues in this region can be OTHER INFORMATION: between three and fourteen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (21)...(27)
OTHER INFORMATION: The number of residues in this region can be OTHER INFORMATION: between three and seven.
APPLICANT: ROBISON, Keith E.
APPLICANT: Millennium Pharmaccuticals Inc.
TITLE OF INVENTION: IDENTIFICATION OF A FAMILY OF SECRETED
TITLE OF INVENTION: DENTIFICATION OF A FAMILY
TITLE OF INVENTION: DROTEINS IN VASCULAR ENDOTHELIUM
FILE REFERENCE: MPI00-048PIRNM
CURRENT APPLICATION NUMBER: 06/16/9876
PRIOR APPLICATION NUMBER: 60/369876
PRIOR FILING DATE: 2003-04-03
PRIOR FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.1
Franchise Of Windows Version 4.0
SEQ ID NO 12
LENGTH: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 26; DB 15; Length 37; 100.0%; Pred. No. 0.51;
                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: VARIANT
LOCATION: 1,3,4
OTHER INFORMATION: The amino acid residue at position 1, 3,
OTHER INFORMATION: be Asp, Glu, Gln or Asn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: consensus
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OTHER INFORMATION: or Asn.
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Best Local Similarity
Matches 10; Conserv
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NAME/KEY: VARIANT
LOCATION: 35
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NAME/KEY: VARIANT
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NAME/KEY: VARIANT
LOCATION: 30
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US-10-231-778-119
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LOCATION: (37)...(37)
COTHER INFORMATION: Xaa=zero or any 1, 2, 3, 4 or 5 amino acids
US-10-386-055-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 26; DB 14; Length 37; 100.0%; Pred. No. 0.51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
          Sequence 41, Application US/10386055
Publication No. US20030186334A1
GENERAL INFORMATION:
APPLICANT: Cezary Marcinkiewicz
TITLE OF INVENTION: KTS-DISINTEGRINS
FILE REFRENCE: 6056-236 C11
CURRENT FILING DATE: 2003-03-11
PRIOR PILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: PCT/US01/28522
PRIOR APPLICATION NUMBER: US 60/231,591
PRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
SSOTUMARE: PastSEQ for Windows Version 4.0
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US-10-406-073-12
; Sequence 12, Application US/10406073
; Sequence 12, Application US/10406073
; Publication No. US20030219813A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Ruey-Bing
; APPLICANT: TOMLINSON, James E.
; APPLICANT: TOMLINSON, James E.
; APPLICANT: TOMPER, James N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (24)...(28)
OTHER INFORMATION: Xaa=any amino acid
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OTHER INFORMATION: Xaa=any amino acid
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LOCATION: (2)...(5)
OTHER INFORMATION: Xaa=any amino acid
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OTHER INFORMATION: Xaa=any amino acid
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OTHER INFORMATION: Xaa=any amino acid
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OTHER INFORMATION: Xaa=any amino acid
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OTHER INFORMATION: Xaa=any amino acid
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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NAME/KEY: VARIANT
LOCATION: (35)...
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GENERAL INFORMATION:

APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Anna M.G.
APPLICANT: Columow, Anna M.G.
APPLICANT: Luo, Ming
APPLICANT: Eacock, William U.G.
ITLE OF INVENTION: Method for inducing seed development by down-regulating
ITLE OF INVENTION: Method for inducing seed development by down-regulating
ITLE OF INVENTION: MARER: US/10/231,778

TITLE OF INVENTION: MARER: US/10/231,778

CURRENT FILING DATE: 1998-09-21

PRIOR FILING DATE: 1998-09-22

PRIOR PELING DATE: 1999-07-01

PRIOR PELING DATE: 1999-07-01
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Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 10; Conservative 0; Mismatches 0; Indels
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CTHER INFORMATION: X at positions 1 to 38 is any amino acid.
US-10-231-778-126
TYPE: PRT ORGANISM: Artificial Sequence FEATURE: OPPERINGE: OTHER INFORMATION: Description of Artificial Sequence: Motif
                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 26; DB 14; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                            FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)..(38)
COTHER INFORMATION: X at positions 1 to 38 is any amino acid.
US-10-231-778-122
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ORGANISM: Artificial Sequence
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geguence 122, Application US/20647A1

general INFORMATION:

GENERAL INFORMATION:

APPLICANT: Bilodeau, Fierre

APPLICANT: Chaudhury, Abdul M.

APPLICANT: Chaudhury, Anna M.G.

APPLICANT: Chaudhury, Anna M.G.

APPLICANT: Chaudhury, Anna M.G.

APPLICANT: Chauchury, Anna M.G.

APPLICANT: Peacock, William J.

ITLE OF INVENTION: expression of the FIS2 gene

FILE REFERENCE: 72-98A

CURRENT FILING DATE: 2002-11-08

PRIOR APPLICATION NUMBER: 09/398,237

PRIOR PILING DATE: 1998-09-22

PRIOR PLING DATE: 1999-07-01

PRIOR PLING DATE: 1999-07-01
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Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: VARIANT
1 LOCATION: (1)..(38)
2 OTHER INFORMATION: X at positions 1 to 38 is any amino acid.
US-10-231-778-119
CURRENT APPLICATION NUMBER: US/10/231,778
CURRENT FILING DATE: 2002-11-08
PRIOR PRIOR FILING DATE: 1999-09-20
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/101,184
PRIOR APPLICATION NUMBER: 60/101,184
PRIOR PILING DATE: 1998-09-22
PRIOR PRILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-22
PRIOR PLING DATE: 1998-09-22
PRIOR PLING DATE: 1998-09-22
PRIOR PLING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-21
PRIOR FILING DATE: 1998-09-21
PRIOR FILING DATE: 1998-09-21
PRIOR FILING DATE: 1998-09-21
PRIOR FILING DATE: 1998-07-01
NUMBER OF SEQ ID NOS: 239
SOFTWARE: PACENTIN VET: 2.0
SENGTH: 38
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SEQ ID NO 122
LENGTH: 38
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FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: VARIANT
LOCATION: (1)..(39)
CTHER INFORMATION: X at positions 1 to 39 is any amino acid
US-10-231-778-123
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Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 10; Conservative 0; Mismatches 0;
                                                       PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: AU PP6063
PRIOR APPLICATION NUMBER: AU PP6063
PRIOR APPLICATION NUMBER: AU P01345
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 239
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 123
LENGTH: 39
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                                 PLICATION NUMBER: AU PP6062
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ORGANISM: Artificial Sequence
FILING DATE: 1998-09-22
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APPLICANT: Bilodeau, Pierre
APPLICANT: Dennis, Elizabeth S.
APPLICANT: Dennis, Elizabeth S.
APPLICANT: Dennis, Elizabeth S.
APPLICANT: Dennis, Filiabeth S.
APPLICANT: Folunow, Anna M.G.
APPLICANT: Encock, William J.
APPLICANT: Peacock, William J.
TITLE OF INVENTION: expression of the FIS2 gene
FILE REFERENCE: 72-98A
CURRENT APPLICATION NUMBER: US/10/231,778
CURRENT APPLICATION NUMBER: 09/398,237
PRIOR APPLICATION NUMBER: 09/398,237
PRIOR FILING DATE: 1999-09-20
SRIOR FILING DATE: 1999-09-21
PRIOR FILING DATE: 1998-09-21
PRIOR FILING DATE: 1998-09-21
PRIOR APPLICATION NUMBER: 60/101,184
PRIOR APPLICATION NUMBER: AU PP6061
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                                                                                                                                  APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Dennis, Elizabeth S.
APPLICANT: Luo, Ming
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100.0%; Score 26; DB 14; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 10; Conservative 0; Mismatches 0; Indels
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; CTHER INFORMATION: X at positions 1 to 38 is any amino acid. US-10-231-778-130
                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE (2-78)
CURRENT PEDICATION NUMBER: US/10/231,778
CURRENT FILING DATE: 2002-11-08
PRIOR FILING DATE: 1999-09-20
PRIOR FILING DATE: 1998-09-20
PRIOR PILING DATE: 1998-09-21
PRIOR PELING DATE: 1998-09-22
PRIOR PELING DATE: 1998-09-22
PRIOR PELING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-22
PRIOR PILING DATE: 1998-09-22
PRIOR PILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 239
SOFTWARRE: PATENT NOW PRIOR PRIOR PELING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 239
SOFTWARRE: PATENT NOW PRIOR PELING DATE: 1999-07-01
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Publication No. US20030126647A1
GENERAL INFORMATION:
                                        Sequence 130, Application US/10231778
Publication No. US20030126647A1
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Gaps

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APPLICANT: Luo, Ming
APPLICANT: Luo, Ming
APPLICANT: Luo, Ming
APPLICANT: Luo, Ming
APPLICANT: Peacock, William J.
ITLE OF INVENTION: Method for inducing seed development by down-regulating
ITTLE OF INVENTION: Method for inducing seed development by down-regulating
ITTLE OF INVENTION: Webser 129-98 ASP 10-231,778
CURRENT FILING DATE: 199-9-9-20
PRIOR APPLICATION NUMBER: 09/398,237
PRIOR FILING DATE: 1998-09-21
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-22
PRIOR PRIOR APPLICATION NUMBER: AU PP6062
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-07-01
PRIOR FILING DATE: 1998-09-07-01
PRIOR FILING DATE: 1998-09-07-01
PRIOR FILING DATE: 1999-07-01
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) OTHER INFORMATION: X at positions 1 to 40 is any amino acid. US-10-231-778-128
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APPLICANT: Yee, David P.
APPLICANT: Pester, Donald C.
APPLICANT: Pester, Donald C.
APPLICANT: Pester, Donald C.
APPLICANT: Pester, Donald C.
APPLICANT: Wo, USZO04066312ZAIAK, Julia E.
APPLICANT: Xu, Wenfeng
APPLICANT: Xa, Yue
TICKON TO TOWNEY TOWER POLYPEPTIDES
FILE REFERENCE: 99-75
CURRENT APPLICATION NUMBER: US/10/660,968
CURRENT APPLICATION NUMBER: US/09/695,369A
PRIOR APPLICATION NUMBER: US/09/695,369A
PRIOR PLING DATE: 1999-10-22
PRIOR FILING DATE: 1999-10-22
PRIOR FILING DATE: 1999-11-02
PRIOR FILING DATE: 1999-11-02
PRIOR FILING DATE: 2000-07-17
PRIOR FILING DATE: 2000-07-17
PRIOR PELING DATE: 2000-07-17
PRIOR PELING DATE: 2000-08-01
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       Koltunow, Anna M.G.
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APPLICANT: Duo, Ming
APPLICANT: Luo, Ming
APPLICANT: Luo, Ming
APPLICANT: Luo, Ming
APPLICANT: Beacock, William J.
TITLE OF INVENTION: Method for inducing seed development by down-regulating
TITLE OF INVENTION: Expression of the FIS2 gene
TITLE OF INVENTION: Expression of the FIS2 gene
TITLE OF INVENTION: Expression of the FIS2 gene
TITLE OF INVENTION: WINBER: 09/10/231,778
CURRENT FILING DATE: 1998-09-22
FRIOR PELICATION NUMBER: 60/101,184
FRIOR FILING DATE: 1998-09-22
FRIOR APPLICATION NUMBER: AU PF6661
FRIOR PELICATION NUMBER: AU PF6663
FRIOR FILING DATE: 1998-09-22
FRIOR APPLICATION NUMBER: AU PF6663
FRIOR FILING DATE: 1998-09-22
FRIOR APPLICATION NUMBER: AU PG1345
FRIOR FILING DATE: 1998-07-01
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                                                                                                     Query Match 100.0%; Score 26; DB 14; Length 39; Best Local Similarity 100.0%; Pred. No. 0.52; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THER INFORMATION: Description of Artificial Sequence: Motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)..(39)
; OTHER INFORMATION: X at positions 1 to 39 is any amino acid. US-10-231-778-129
; OTHER INFORMATION: X at positions 1 to 39 is any amino acid. US-10-231-778-127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 26; DB 14; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 10; Conservative 0; Mismatches 0; Indels
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. Sequence 129, Application US/10231778
. Publication No. US20030126647A1
. CENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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100.0%; Score 26; DB 13; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                         Query Match
100.0%; Score 26; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/10006467;
Sequence 8, Application VS/10006467;
Publication No. US20020164740A1
GENERAL INFORMATION:
FAPPLICANT: HOlloway, James L.
TITLE OF INVENTION: Scys5: A Member of the Cystatin
TITLE OF INVENTION: Superfamily
FILE REPERENCE: 99-104C1
CURRENT FILING DATE: 2001-12-04
FRIOR FILING DATE: 2001-12-04
FRIOR FILING DATE: 1999-12-23
FRIOR APPLICATION NUMBER: 09/740,638
FRIOR FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PastSEQ for Windows Version 3.0
FRIOR PARCEL FARMED FOR THE SEQ ID NOS: 13
SOFTWARE: PastSEQ for Windows Version 3.0
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; Publication No. US20030100096A1
; GENERAL INFORMATION:
; APPLICANT: Holloway, James L.
; TITLE OF INVENTION: 2cys5: A Member of the Cystatin, TITLE OF INVENTION: Superfamily
; FILE REPERSINCE: 99-104C1
; CURRENT RILING DATE: 2002-09-04
; PRIOR FILING DATE: 1999-12-23
; PRIOR FILING DATE: 2002-09-04
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 13
; SOFFWARE: FartSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH; 43
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LOCATION: (1)...(43)

COTHER INFORMATION: Xaa is any amino acid.

19.-10-006-467-8
                                                  FEATURE:
COTHER INFORMATION: Motif
NAME/KEY: VARIANT
LOCATION: (1) ... (43)
CTHER INFORMATION: Xaa is any amino acid.
US-09-740-638-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Motif
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OTHER INFORMATION: Bach Xaa is independently any amino acid residue
FEATURE:
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LOCATION: (27)...(30)
OTHER INFORMATION: Each Xaa is independently any amino acid residue
OTHER INFORMATION: or not present
FEATURE:
NAME/KEY: VARIANT
LOCATION: (32)...(37)
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OTHER INFORMATION: Each Xaa is independently any amino acid residue OTHER INFORMATION: or not present
                                                                                                                                                                                                                                                                                   FEATURE:
NAMPIGENTANT
LOCATION: (3)...(12)
OTHER INFORMATION: Each Xaa is independently any amino acid residue
FEATURE:
NAME/KEY: VARIANT
LOCATION: (13)...(16)
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OTHER INFORMATION: Each Xaa is independently any amino acid residue OTHER INFORMATION: or not present
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NAME/KEY: VARIANT
OCCATION: (19)...(20)
OTHER INFORMATION: Each Xaa is independently any amino acid residue
FEATURE:
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (13)...(16)
OTHER INFORMATION: Each Xaa is independently any amino acid residue
OTHER INFORMATION: or not present
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100.0%; Score 26; DB 12; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 10; Conservative 0; Mismatches 0; Indels
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US-09-740-638-8

US-09-740-638-8

Sequence 8, Application US/09740638

Patent No. US2020006665A1

GENERAL INFORMATION:
APPLICANT: HOlloway, James L.
TITLE OF INVENTION: Superfamily
TITLE OF INVENTION: Superfamily
FILE REFERENCE: 99-104

CURRENT FILING DATE: 2000-12-18

CURRENT FILING DATE: 2000-12-18

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 8

LENDTH: 43

TYPE: PRI
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. TOTHER INFORMATION: Xaa is any amino acid residue
US-10-660-968-4
                                                                                                                                                                                                         NAME/KEY: VARIANT
LOCATION: (1)...(1)
OTHER INFORMATION: Xaa is any amino acid residue
SEQ ID NO 4
LENGTH: 41
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Pseudo repeat motif #1
FEATURE:
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NAME/KEY: VARIANT
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NG-10-180-247-15

Sequence 15, Application US/10180247

Sequence 15, Application US/10180247

Publication No. US20030167519A1

GENERAL INFORMATION:
APPLICANT: DeRose, Richard
APPLICANT: Freysinnet, Georges
APPLICANT: Hoffman, Jules
TITLE OF INVENTION: Chimeric Gene Encoding Drosomycin,
TITLE OF INVENTION: Vector Containing It and Production of Disease-Resistant
TITLE OF INVENTION: Vector Containing It and Production of Disease-Resistant
TITLE OF INVENTION: Vector Containing It and Production of Disease-Resistant
TITLE OF INVENTION: Vector Containing It and Production of Disease-Resistant
TITLE OF INVENTION: Vector Containing It and Production of Disease-Resistant
TITLE OF INVENTION WHERE: USA-A-A 072667.0182
CURRENT FILING DATE: 2002-06-26

PRIOR APPLICATION NUMBER: PCT/FP99/01462

PRIOR FILING DAIE: 1998-07-08

PRIOR FILING DAIE: 1998-07-08

PRIOR FILING DAIE: 1998-07-08
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100.0%; Score 26; DB 14; Length 44;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 10; Conservative 0; Mismatches 0; Indels
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Sequence 9, Application US/10235148
Publication No. US20030100096A1
GENERAL INFORMATION:
TITLE CAPELICANT: HOLICWAY, James L.
TITLE OF INVENTION: Superfamily
TITLE OF INVENTION: Superfamily
FILE REFERENCE: 99-104C1
CURRENT FILING DATE: 2002-09-04
PRIOR FILING DATE: 2002-09-04
PRIOR FILING DATE: 2002-09-04
PRIOR FILING DATE: 2000-12-13
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
LENGTH: 44
                                                                                                                                                                                                                                                                                                                   Mismatches
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NAME/KEY: VARIANT
LOCATION: (1)...(44)
OTHER INFORMATION: Xaa is any amino acid. US-10-235-148-9
           ) OTHER INFORMATION: Motif

NAME/KEY: VARIANT

LOCATION: (1) ... (44)

OTHER INFORMATION: Xaa is any amino acid.

US-10-006-467-9
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 10; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 10; Conservative 0; Mismatches 0; Indels
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Sequence 9, Application US/10006467

Publication No. US20020164740A1

GENERAL INFORMATION:

TITLE OF INVENTION: Superfamily

FILE REFERENCE: 99-104C1

CURRENT FULICATION NUMBER: US/10/006,467

CURRENT FILING DATE: 2001-12-04

PRIOR APPLICATION NUMBER: 60/172,119

PRIOR FILING DATE: 1999-12-23

PRIOR PILING DATE: 1999-12-23

PRIOR PILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-70-638-9; Sequence 9, Application US/09740638; Sequence 9, Application US/09740638; Patent No. US2002006656A1; Patent No. US2020006565A1; TITLE OF INVENTION: Zcy85: A Member of the Cystatin; TITLE OF INVENTION: Superfamily; FILE REFERENCE: 99-104; CURRENT FILIG DATE: 2000-12-18; NUMBER OF SEQ ID NOS: 13; SOFTWARE: PastSEQ for Windows Version 3.0; SEQ ID NO 9; S
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: VARIANT
LOCATION: (1)...(44)
CTHER INFORMATION: Xaa is any amino acid. (25-09-740-638-9
                                                                                                                                                     ; FEATURE:

NAME/KEY: VARIANT

; LOCATION: (1)...(43)

; OTHER INFORMATION: Xaa is any amino acid.
US-10-235-148-8
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Motif
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OTHER INFORMATION: Preferably Ser Gly Arg Tyr Lys Gly
                                                                                                                                                                                                 OTHER INFORMATION: Drosomycin Core Sequence
PRIOR FILING DATE: 1997-07-11
PRIOR APPLICATION NUMBER: FR97/09,663
PRIOR FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 44
                                                                                                                                                                                                              FEATURE:
NAME/KEY: VARIANT
OTHER INFORMATION: Preferably Asp
FEATURE:
NAME/KEY: VARIANT
LOCATION: (3)...(3)
OTHER INFORMATION: Preferably Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: VARIANT
LOCATION: (42) ... (42)
OTHER INFORMATION: Preferably Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: VARIANT
COCATION: (40)
THER INFORMATION: Preferably Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: VARIANT
LOCATION: (43)...(43)
OTHER INFORMATION: Preferably Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'FATURE:
ADME/KEY: VARIANT
JOCATION: (34)...(34)
OTHER INFORMATION: Preferably Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AME/KEY: VARIANT
CCATION: (38)...(38)
THER INFORMATION: Preferably Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (24)...(24)
OTHER INFORMATION: Preferably Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OCATION: (32)...(32)
THER INFORMATION: Preferably His
                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: VARIANT
CLCATION: (10)...(10)
CTHER INFORMATION: Preferably Pro
FEATURE:
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COCATION: (18)...(18)
THER INFORMATION: Preferably Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OCATION: (20)...(20)
THER INFORMATION: Preferably Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RME/KEY: VARIANT
OCATION: (22)...(22)
THER INFORMATION: Preferably Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (12)...(12)
DTHER INFORMATION: Preferably Ala
                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REATURE:
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0
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 10; Conservative 0; Mismatches 0; Indels
LOCATION: (13)...(17)
PURE INFORMATION: Preferably Val Trp Asp Asn Glu
PEATURE:
NAME/KEY: VARIANT
COCATION: (21)...(21)
COCATION: (21)...(21)
FEATURE:
NAME/KEY: VARIANT
NAME/KEY: VARIANT
NAME/KEY: VARIANT
NAME/KEY: VARIANT
NAME/KEY: (25)...(31)
COCATION: (25)...(31)
COCATION: (25)...(31)
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Patent No. US20020102703A1

GENERAL INFORMATION:

APPLICANT: Box, Brian A.

TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE ZKUNIO

TITLE REPRESENCE: 99-84

CURRENT FILING DATE: 2000-12-28

PRIOR FILING DATE: 1999-12-29

NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09794589

Sequence 7, Application US/09794589

Patent No. US20020004224A1

GENERAL INFORMATION:
TITLE OF INFORMATION:
FILE REFERENCE: 00-01

CURRENT APPLICATION WHERE: US/09/794,589

CURRENT FILING DATE: 2001-02-27

PRIOR APPLICATION NUMBER: US 60/186,069

PRIOR FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatesEQ for Windows Version 3.0

SEQ ID NO 7;
                                                                                                                                                                                                                  FEATURE:
NAME/KEY: VARIANT
LOCATION: (35)...(37)
OTHER INFORMATION: Preferably Pro Ser Leu
US-10-180-247-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
COGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: kunitz motif
NAME/KEY: VARIANT
COCATION: (1)...(51)
COCATION: (1)...(51)
US-09-794-589-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CXXXXXXXC 10
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US-09-750-964-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 85
US-09-794-589-7
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is any residue except Cys, His, Ile, Phe, Pro, Thr, Trp, ?
                                                                                                                                                                                                                                                                                                 LOCATION: (25)...(25)
OTHER INFORMATION: Xaa is any residue except Asn, Asp, Cys, His, Ile, Pro, Trp, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OCATION: (28)...(28)
THER INFORMATION: Xaa is any residue except Asp, Cys, His, Ile, Phe, Trp or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OCATION: (48)....(48)
THER INFORMATION: Xaa is any residue except Ala, Cys, Gly, Phe, Pro, Ser, Thr,
AME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pro
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                                                                                                                                          Tyr or Val
                                                                                                                                                                                                                                                                                                                                                                                            OCATION: (27)...(27)
OTHER INFORMATION: Xaa is any residue except Cys, Gly, Phe, Pro, Ser or Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arg or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AME/KEY: VARIANT

OCCATION: (35)...(35)

THER INFORMATION: Xaa is Gly, Lys, Arg, Pro, Gln, Leu, Glu, Asn or Met

RAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 residue except Cys, Gln, Gly, Phe or Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lys,
                                                                                                                                          Thr, Ile, Gln, Glu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ION: (30)...(30) INFORMATION: Xaa is any residue except Arg, Cys, Gly or Met
            LOCATION: (22)...(22)
OTHER INFORMATION: Xaa is any residue except Cys, Met, Pro or Trp
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tyr or Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gln,
                                                                                                                                                                                                 LOCATION: (24)...(24)
OTHER INFORMATION: Xaa is Lys, Gln, Asn, His, Gly, Arg or Met
NAME/KEY: VARIANT
LOCATION: (25)...(25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Val,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEY: VARIANT
TION: (40) ... (40)
? INFORMATION: Xaa is Arg, Asn, Lys, Gln or Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lys or Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Met,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phe or Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            His,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lys, Gln, Asp,
                                                                                                                                                Ser, Leu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEXEY: VARIATION: Add is ris, if the region of the recognition (42)...(42)
CATION: (42)...(42)
MEXER: VARIANT
CATION: (43)...(43)
MEXER: VARIANT
HER INFORMATION: Add is Thr, Ser, Arg, Ly
MEXEX: VARIANT
HER INFORMATION: Add is Ile, Leu, Trp, Ar
MEXEX: VARIANT
MEXEX: VARIANT
HER INFORMATION: Add is Ile, Leu, Trp, Ar
MEXEX: VARIANT
HER INFORMATION: Add is Glu, Asp, Ala, Hi
MEXEX: VARIANT
MEXEX: VARIANT
HER INFORMATION: Add is Glu, Lys, Gln, As
MEXEX: VARIANT
MEXEX: VARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lys or Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ION: (32)...(32)
INFORMATION: Xaa is Ser, Gly or Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TION: (36)...(36)
R INFORMATION: Xaa is Gly, Lys or Ala
/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tyr or Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEY: VARIANT
11ON: (39)...(39)
! INFORMATION: Xaa is Asn or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: VARIANT
LOCATION: (33)...(33)
DTHER INFORMATION: Xaa is Gly or ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AME/KEY: VARIANT
OCATION: (31)...(31)
OTHER INFORMATION: Xaa is Tyr, Trp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phe or Tyr
                                                                                                                LOCATION: (23)...(23)
OTHER INFORMATION: Xaa is Ala, Lys,
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITON: (37)...(37)
ER INFORMATION: Xaa is Asn, L;
2/KEY: VARIANT
STION: (38)...(38)
ER INFORMATION: Xaa is any re-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YEY: VARIANT
FION: (41)...(41)
R INFORWATION: Xaa is Phe,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ON: (29)...(29)
INFORMATION: Xaa is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: VARIANT
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                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: VARIANT
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LOCATION: (15)
LOCATION: (15)
NAME/KEY: VARIANT
LOCATION: (17)
NAME/KEY: VARIANT
LOCATION: (17)
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trp or Ty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OCATION: (14)...(14)
THER INFORMATION: Xaa is any residue except Arg, Asn, Cys, Gly, His, Ser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (20)...(20)
OTHER INFORMATION: Xaa is Lys, Asn, Ser or Asp
MAME/KEY: VARIANI
LOCATION: (21)...(21)
OTHER INFORMATION: Xaa is any residue except Asp, Cys, Glu, His or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (6)....(6)
OTHER INFORMATION: Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, Tyr
NAMESKRY: VARIANT
TOCHER INFORMATION: OF Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPINE: (7)....(7)
OTHER INFORMATION: Xaa is any residue except Asn, Cys, Gly, His, Leu,
OTHER INFORMATION: Met, Phe or Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JUCATION: (11)...(11)

THER INFORMATION: Xaa is any residue except Ala, Cys, Glu, His, Ile, AME, KEY: VARIANT

AME, KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trp,
                                                                                                                                                                                                                                                                           residue except Asp, Cys, Gly, His, Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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THER INFORMATION: Xaa is Arg, Lys, Ala, Asp, Gln, Phe, Gly, Glu,
THER INFORMATION: or Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Asn
                                                                                                                                                                                                                                                                                                                                                                                                  Thr, Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phe,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IAME/KEY: VARIANT
JOCATION: (13)...(13)
THER INFRMATION: Xaa is any residue except Asp, Cys, Glu, Pro
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gly,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Val, Ser, Asp, Ile,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (4)...(4)
OTHER INFORMATION: Xaa is any residue except Arg, Cys, Met,
OTHER INFORMATION: Tyr or Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gln,
                                                                                                                                                                                                                                                                                                                                                               LOCATION: (3)...(3)
OTHER INFORMATION: Xaa is Leu, Glu, Met, Gln, Phe, Ser,
OTHER INFORMATION: Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4 LENGTH: 51 TYPE: PRT ORGANISM: Artificial Sequence FRACHISM: OTHER INFORMATION: kunitz motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCATION: (9)...(9)
HER INFORMATION: Xaa is Pro, Arg, Leu,
THER INFORMATION: Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCATION: (19)...(19)
DTHER INFORMATION: Xaa is Tyr or Phe
AAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: VARIANT
LOCATION: (8)...(8)
OTHER INFORMATION: Kaa is Gly or Glu
                                                                                                                                                                                                              NAME/KEY: VARIANT
LOCATION: (2)...(2)
OTHER INFORMATION: Xaa is any
OTHER INFORMATION: Pro or Trp
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: VARIANT
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NAMES/KEY: VARIANT
LOCATION: (14)...(14)
LOCATION: (15)...(15)
OTHER INFORMATION: Xaa is any residue except Arg, Asn, Cys, Gly, His, Ser, OTHER INFORMATION: Trp or Tyr
NAMES/KEY: VARIANT
LOCATION: (15)...(15)
OTHER INFORMATION: Xaa is any residue except Ala, Asp, Cys, Gly, His, Met, OTHER INFORMATION: Trp or Tyr
NAMES/KEY: VARIANT
LOCATION: (16)...(16)
OTHER INFORMATION: Xaa is Ser, Ala, Arg, Val, Gln, Lys, Leu, Gly or Ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT

LOCATION: (8) ...(8)

OTHER INFORMATION: Xaa is Gly or Glu

NAME/KEY: VARIANT

LOCATION: (9) ...(9)

OTHER INFORMATION: Xaa is Pro, Arg, Leu, Val, Ser, Asp, Ile, Asn or OTHER INFORMATION: Thr

NAME/KEY: VARIANT

LOCATION: (11) ...(11)

OTHER INFORMATION: Xaa is any residue except Ala, Cys, Glu, His, Ile, OTHER INFORMATION: Pro, Trp or Val

LOCATION: (12) ...(12)

OTHER INFORMATION: Xaa is Arg, Lys, Ala, Asp, Gln, Phe, Gly, Glu, Thr

OTHER INFORMATION: Or Ser

NAME/KEY: VARIANT

LOCATION: (13) ...(12)

OTHER INFORMATION: Xaa is Arg, Lys, Ala, Asp, Gln, Phe, Gly, Glu, Thr

OTHER INFORMATION: Asa is any residue except Asp, Cys, Glu, Pro or Thr

NAME/KEY: VARIANT

LOCATION: (13) ...(13)

OTHER INFORMATION: Xaa is any residue except Asp, Cys, Glu, Pro or Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (22)...(22)
OTHER INFORMATION: Xaa is any residue except Cys, Met, Pro or Trp
NAME/REY: VARTANT
LOCATION: (23)...(23)
OTHER INFORMATION: Xaa is Ala, Lys, Ser, Leu, Thr, Ile, Gln, Glu, Tyr or
OTHER INFORMATION: Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT
LOCATION: (19)
OTHER INPORMATION: Xaa is Tyr or Phe
NAME/KEY: VARIANT
LOCATION: (20)
OTHER INPORMATION: Xaa is Lys, Asn, Ser or Asp
NAME/KEY: VARIANT
NAME/KEY: VARIANT
NAME/KEY: VARIANT
OTHER INPORMATION: Xaa is any residue except Asp, Cys, Glu, His or Tyr
NAME/KEY: VARIANT
NAME/KEY: VARIANT
NAME/KEY: VARIANT
                                                                                                                                                 Phe, Trp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOUN: (')...(') Xaa is any residue except Asn, Cys, Gly, His, Leu, INFORMATION: Met, Phe or Trp
                                       or
      LOCATION: (3)...(3)
OTHER INFORMATION: Xaa is Leu, Glu, Met, Gln, Phe, Ser, Thr, Ala
OTHER INFORMATION: Pro
                                                                                                                                                                                                                                       ION: (5)...(5)
INFORMATION: Xaa is any residue except Asn, Cys, Gln, Gly,
INFORMATION: Ser, Thr or Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: VARIANT
LOCATION: (24)...(24)
OTHER INFORMATION: Xaa is Lys, Gln, Asn, His, Gly, Arg or Met
                                                                                                                                                                                                                                                                                                                   NAME/KEY: VARIANT
LOCATION: (6)...(6)
OTHER INFORMATION: Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys,
OTHER INFORMATION: or Met
LOCATION: (7)...(7)
                                                                                                                                                 residue except Arg, Cys, Met,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: VARIANT
LOCATION: (18)...(18)
OTHER INFORMATION: Xaa is Tyr, His, Phe, Trp, Asn or Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trp or Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: VARIANT
LOCATION: (17)...(17)
OTHER INFORMATION: Xaa is Phe,
                                                                                                                      LOCATION: (4)...(4)
OTHER INFORMATION: Xaa is any
OTHER INFORMATION: Tyr or Val
                                                                                                                                                                                                           NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER

b LOCATION: (49)...(49)
c OTHER INFORMATION: Xaa is any residue except Cys, Ile, Leu, Met, Phe, Pro, Ser, Tyr
nAME/KEX: VARIANT
LOCATION: (50)...(50)
c OTHER INFORMATION: Xaa is Thr, Ala, Val, Ile, Phe, Leu, Met, Lys, Tyr or Arg
US-09-750-964-4
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OTHER INFORMATION: Xaa is any residue except Asp, Cys, Gly, His, Met,
OTHER INFERMATION: Pro or Trp
NAME/KEY: VARIAN:
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Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 26; DB 9; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 87
US-09-740-510-5
; Sequence 5, Application US/09740510
; Patent No. US20020111460A1
; GENERAL INFORMATION:
; APPLICANT: HOLLOWAY, James L.
; TITLE OF INVENTION:
; TILE REFERENCE: 99-103
; CURRENT APPLICATION NUMBER: US/09/740,510
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 3.0
; LENGTH: 51
; TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-10-1963-3

// Sequence 3, Application US/10021963

// Sequence 3, Application US/10021963

// Publication No US20020110887A1

// GENERAL INFORMATION:

// TITLE OF INVENTION: KUNITZ DOWAIN POLYPEPTIDE ZKUNG

// TITLE OF INVENTION: KUNITZ DOWAIN POLYPEPTIDE ZKUNG

// CURRENT APPLICATION NUMBER: US/10/021,963

// CURRENT FILING DATE: 2001-12-14

// PRIOR APPLICATION NUMBER: US/99/388,183

// PRIOR FILING DATE: 1999-0-01

// NUMBER OF SEQ ID NOS: 7

// SOFTWARE: FastSEQ for Windows Version 3.0

// SEQ ID NO 3

// LENGTH: 51

// TWOE: DOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1)...(51)
OTHER INFORMATION: Xaa is any amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Kunitz motif
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
OTHER INFORMATION: motif.
NAME/KEY: VARIANT
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) OTHER INFORMATION: Ser, Tyr or Val

) NAME/KEY: VARIANT

) LOCATION: (50)...(50)

) OTHER INFORMATION: Xaa is Thr, Ala, Val, Ile, Phe, Leu, Met, Lys, Tyr or

) OTHER INFORMATION: Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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100.0%; Score 26; DB 14; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 10; Conservative 0; Mismatches 0; Indels
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Sequence 5, Application US/10225261

Sequence 5, Application WS/10225261

Publication No. US20030100070A1

GENERAL INFORMATION:

APPLICANT: Holloway, James L.

TITLE OF INVENTION: Kunitz Domain Polypeptide Zkunl1

FILE REPERENCE: 99-103

CURRENT RILING DATE: 2002-08-20

CURRENT FILING DATE: 2002-08-20

NUMBER OF SEC 1D NOS: 12

SOFTWARE: FRALESE for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: VARIANT

LOCATION: (1)...(51)

COTHER INFORMATION: Xaa is any amino acid.

WS-10-225-261-5
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ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Kunitz motif
PEATURE:
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: motif.
FEATURE:
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LENGTH: 51
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LOCATION: (49)...(49)
OTHER INFORMATION: Xaa is any residue except Cys, Ile, Leu, Met, Phe, Pro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OCATION: (48)...(48)
THER INFORMATION: Xaa is any residue except Ala, Cys, Gly, Phe, Pro, Ser,
THER INFORMATION: Thr, Trp or Tyr
                                 LOCATION: (25)
OTHER INFORMATION: Xaa is any residue except Asn, Asp, Cys, His, Ile, Pro, OTHER INFORMATION: Trp, Tyr or Val
NAME/KEY: VARIANT
LOCATION: (27)...(27)
OTHER INFORMATION: Xaa is any residue except Cys, Gly, Phe, Pro, Ser or OTHER INFORMATION: Trp
NAME/KEY: VARIANT
LOCATION: (28)...(28)
OTHER INFORMATION: Xaa is any residue except Asp, Cys, His, Ile, Phe, Trp
OTHER INFORMATION: Xaa is any residue except Asp, Cys, His, Ile, Phe, Trp
NAME/KEY: VARIANT
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCATION: (38)...(38)
HER INFORMATION: Xaa is any residue except Cys, His, Ile, Phe, Pro, Thr,
HER INFORMATION: Trp, Tyr or Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (45)...(45)
OTHER INFORMATION: Xaa is Glu, Asp, Ala, His, Met, Val, Gln, Lys, Arg or
OTHER INFORMATION: Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OCCATION: (44)...(44)
THER INFORMATION: Xaa is Ile, Leu, Trp, Arg, Lys, Thr, Glu, Ala, Gln or
THER INFORMATION: Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AME/KEY: VARIANT
OCATION: (35)...(35)
THER INFORMATION: Xaa is Gly, Lys, Arg, Pro, Gln, Leu, Glu, Asn or Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AWE/KEY: VARIANT
OCATION: (41)
TCHER INFORMATION: Xaa is Phe, Tyr or Asp
NAME/KEY: VARIANT
OCATION: (42)
THER INFORMATION: Xaa is any residue except Cys, Gln, Gly, Phe or Trp
                                                                                                                                                                                                                                                                                                                                                                        COCATION: (30)...(30)
THER INFORMATION: Xaa is any residue except Arg, Cys, Gly or Met
AAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (46)...(46)
OTHER INFORMATION: Xaa is Glu, Lys, Gln, Asp, Ala, Tyr or Ser
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (43)...(43)
OTHER INFORMATION: Xaa is Thr, Ser, Arg, Lys or Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ION: (40)...(40)
INFORMATION: Xaa is Arg, Asn, Lys, Gln or Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                 OCATION: (31)...(31)
THER INFORMATION: Xaa is Tyr, Trp, Phe or Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OCATION: (36)...(36)
THER INFORMATION: Xaa is Gly, Lys or Ala
AME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OCATION: (37)...(37)
THER INFORMATION: Xaa is Asn, Lys or Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OCATION: (32)...(32)
THER INFORMATION: Xaa is Ser, Gly or Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OCATION: (33)...(33)
THER INFORMATION: Xaa is Gly or Ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ION: (39)...(39)
INFORMATION: Xaa is Asn or Tyr
                                                                                                                                                                                                                                                                                                              LOCATION: (29)...(29)
OTHER INFORMATION: Xaa is Phe or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AME/KEY: VARIANT
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              NAME/KEY: VARIANT
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FEATURE:
NAME/KEY: VARIANT
LOCATION: (27)...(27)
OTHER INFORMATION: Kaa is any residue except Asn, Asp, Cys, His, Ile, Pro, Trp, '
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OTHER INFORMATION: Xaa is any residue except Ala, Asp, Cys, Gly, His, Met, Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (15)...(15)
OTHER INFORMATION: Xaa is any residue except Arg, Asn, Cys, Gly, His, Ser, Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ile, Gln, Glu, Tyr or Val
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LOCATION: (28)...(28)
OTHER INFORMATION: Xaa is any residue except Cys, Gly, Phe, Pro, Ser or Trp
FEATURE:
LOMB KEY: VARIANT
LOCATION: (29)...(29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                val, Gln, Lys, Leu, Gly or Ile
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LOCATION: (22)...(22)
DIHER INFORMATION: Xaa is any residue except Asp, Cys, Glu, His or Tyr
                                                                                                                                                                                                                                                                                                                                                    LOCATION: (14)...(14)
OTHER INFORMATION: Xaa is any residue except Asp, Cys, Glu, Pro or Thr
                                                                                                                                                                                                                           LOCATION: (13)...(13)
OTHER INFORMATION: Xaa is Arg, Lys, Ala, Asp, Gln, Phe, Gly, Glu, Thr
OTHER INFORMATION: or Ser
                                                                                                                           LOCATION: (12)...(12)
OTHER INFORMATION: Xaa is any residue except Ala, Cys, Glu, His, Ile,
OTHER INFORMATION: Pro, Trp or Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME: CASI...(25)
LOCATION: (25)...(25)
OTHER INFORMATION: Xaa is Lys, Gln, Asn, His, Gly, Arg or Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ION: (23)...(23)
INFORMATION: Xaa is any residue except Cys, Met, Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OCTION: (19)...(19)
THER INFORMATION: Xaa is Tyr, His, Phe, Trp, Asn or Ala
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thr,
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NAME/KEY: VARIANT
LOCATION: (24)...(24)
OTHER INFORMATION: Xaa is Ala, Lys, Ser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OCATION: (17)...(17)
)THER INFORMATION: Xaa is Ser, Ala, Arg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tyr, Ile,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is Tyr or Phe
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THER INFORMATION: Xaa is Phe,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COCATION: (20)...(20)
OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: VARIANT
COCATION: (21)
THER INFORMATION: Xaa
                                       LOCATION: (11)...(11)
OTHER INFORMATION: Thr
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MAE/KEY: VARIANT
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NAME/KEY: VARIANT
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NAME/KEY: VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ION: (2) ... (2) INFORMATION: Xaa is any residue except Asp, Cys, Gly, His, Met,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAME/KEY: VARIANT
LOCATION: (5)...(5)
OTHER INFORMATION: Xaa is any residue except Arg, Cys, Met, Phe, Trp,
OTHER INFORMATION: Tyr or Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: VARIANT
LOCKTRON: (6)...(6)
OTHER INFORMATION: Xaa is any residue except Asn, Cys, Gln, Gly, Phe,
OTHER INFORMATION: Ser, Thr or Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: VARIANT
COCATION: (9)...(9)
COTER INFORMATION: Xaa is Gly or Glu
COTHER INFORMATION: Xaa is Pro, Arg, Leu, Val, Ser, Asp, 11e, Asn or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (3)...(3)
OTHER INFORMATION: Pro or Trp
OTHER INFORMATION: Xaa is Leu, Glu, Met, Gln, Phe, Ser, Thr, Ala
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lyв,
                                                                                        DB 14; Length 51;
                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Val, Asp,
                                                                                                                                                                                                                                                                              RESULT 91
US-10-115-43-4

i Sequence 4, Application US/10315432

sequence 4, Application US/10315432

publication No. US203016225941

i GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE ZKUNIO
FILE REFERENCE: 99-84

CURRENT FILING DATE: 2002-12-09

PRIOR FILING DATE: 2000-12-28

PRIOR FILING DATE: 1999-12-29

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 3:0

LENGTH: 51
                                                                                               . 0.56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (7)....(7)
OTHER INFORMATION: Xaa is Arg, Glu, Asn, Ala,
                                                                                      Query Match
100.0%; Score 26; DB
Best Local Similarity 100.0%; Pred. No. 0.5
Matches 10; Conservative 0; Mismatches
; LOCATION: (1)...(51)
; OTHER INFORMATION: Xaa = Any Amino Acid US-10-315-380-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: Kunitz motif
NAME/KEY: VARIANT
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ORGANISM: Artificial Sequence
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NAME/KEY: VARIANT
LOCATION: (4) ... (4)
OTHER INFORMATION: Pro
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NAME/KEY: VARIANT
LOCATION: (8)...(8
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NAME/KEY: VARIANT
LOCATION: (3)...(5
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Sequence 8, Application US/09874056
; Sequence 8, Application US/09874056
; Publication No. US20020192704A1
; GENERAL INFORMATION:
; APPLICANT: OKANO, Akira
; APPLICANT: ETO, Yuzuru
; APPLICANT: IZUMI, Tetsuuc
; TITLE OF INVENTION: Same
; TITLE OF INVENTION: Same
; TITLE OF INVENTION: Same
; FILE REFERENCE: 2004-27050
; CURRENT FILING DATE: 2001-06-06
; PRIOR PILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENTER: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAME/KEY: MISC FEATURE LOCATION: (16) ... (16) ... (16) ... (18) ... IS ANY AMINO ACID OR NONEXISTENT
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SR INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
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THER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT EATURE:
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OTHER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
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OTHER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
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OTHER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
PRATURE:
NAME/KEY: MISC_FEATURE
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THER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
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THER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
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LOCATION: (7)...(7)
DTHER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
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OCATION: (12) ..(12)
THER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
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NAME/KEY: MISC_FEATURE
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NAME/KEY: MISC FEATURE
LOCATION: (3). (3)
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ORGANISM: Mus musculus
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INFORMATION: Xaa is any residue except Cys, His, Ile, Phe, Pro, Thr, Trp, Tyr
OTHER INFORMATION: Xaa is any residue except Asp, Cys, His, Ile, Phe, Trp or Tyr
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NAME/KEY: VARIANT
LOCATION: (46)...(46)
OTHER INFORMATION: Xaa is Glu, Asp, Ala, His, Met, Val, Gln, Lys, Arg or Pro
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OTHER INFORMATION: Xaa is Ile, Leu, Trp, Arg, Lys, Thr, Glu, Ala, Gln or Val
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THER INFORMATION: Xaa is Gly, Lys, Arg, Pro, Gln, Leu, Glu, Asn or Met
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THER INFORMATION: Xaa is any residue except Cys, Gln, Gly, Phe or Trp
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                                                                                                                                    NAME/KEY: VARIANT
LOCATION: (31)...(31)
OTHER INFORMATION: Xaa is any residue except Arg, Cys, Gly or Met
FEBATURE:
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OTHER INFORMATION: Xaa is Glu, Lys, Gln, Asp, Ala, Tyr or Ser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OCATION: (41)...(41)

THER INFORMATION: Xaa is Arg, Asn, Lys, Gln or Val
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                                                                                                                                                                                                                                                          LOCATION: (32)...(32)
OTHER INFORMATION: Xaa is Tyr, Trp, Phe or Asp
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THER INFORMATION: Xaa is Phe, Tyr or Asp
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HER INFORMATION: Xaa is Asn, Lys or Ser
                                                                                                                                                                                                                                                                                                                                                                          is Ser, Gly or Thr
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THER INFORMATION: Xaa is Thr, Ser, Arg,
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OCATION: (35)...(35)
)THER INFORMATION: Xaa is Gly or Ile
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HER INFORMATION: Xaa is Asn or Tyr
                                                                                            Phe or Tyr
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THER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCATION: (37)...(37)
THER INFORMATION: Xaa
                                                                      LOCATION: (30)...(30)
OTHER INFORMATION: Xaa
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AME/KEY: VARIANT
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AME/KEY: VARIANT
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AME/KEY: VARIANT
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                           FEATURE:
NAME/KEY: VARIANT
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THER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT

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AME/KEY: MISC FEATURE
OCATION: (37) ... (37)
THER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
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(43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... (43) ... 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(43) ... (43) ... (43) ... (43
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AME/KEX: MISC_FEATURE
OCATION: (28)...
THER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
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THER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
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TTHER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
FATURE:
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NAME/KEY: MISC_FEATURE
LOCATION: (19): (19)
OTHER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
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LOCATION: (20)...(20)
OTHER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
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OCATION: (23) ... (23)
OTHER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
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THER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
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INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
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THER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
LOCATION: (17)..(17)

THER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
                                                                                                                                                                  NAME/KEY: MISC FEATURE
LOCATION: (18) ... (18)
OTHER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
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HERE INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
PATURE:
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THER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
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THER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
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AME/KEY: MISC_FEATURE
OCATION: (42)...(42)
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ORGANISM: Artificial Sequence
FEATURE:
OFFER INFORMATION: peptide motif
NAME/KEY: VARIANT
LOCATION: (2) ... (7)
OTHER INFORMATION: Xaa = any amino acid
NAME/KEY: VARIANT
LOCATION: (8) ... (9)
OTHER INFORMATION: Xaa = any amino acid or is not present
LOCATION: (11) ... (25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09819136
) Batent No. US20020146789A1
) GENERAL INFORMATION
) APPLICANT: Gao, Zeren
) TITLE OF INVENTION: MULTI-DOMAIN PROTEINASE INHIBITOR
) TITLE OF INVENTION: MULTI-DOMAIN PROTEINASE INHIBITOR
) CURRENT APPLICATION NUMBER: US/09/819,136
) CURRENT FILING DATE: 2001-03-27
) PRIOR APPLICATION NUMBER: US 60/193,642
) PRIOR APPLICATION NUMBER: US 60/193,642
) PRIOR APPLICATION NUMBER: US 60/193,642
) RIOR APPLICATION NUMBER: US 60/193,642
) RECORMARE: FARENCE CON ON S: 13
) NUMBER OF SEQ ID NOS: 13
) SEQ ID NO 5:
IENGTH: 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (52)...(52)
FEATURE INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
FEATURE:
                                                                                                                                                                                                                                                                           NAME/KEY: MISC_FEATURE
LOCATION: (49)...(49)
OTHER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
FEATURE:
NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (50) ... (50) OTHER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MISC_FEATURE
LOCATION: (45)...(45)
COTHER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
FEATURE:
NAME/KEY: MISC_EATURE
LOCATION: (47)...(47)
OTHER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
                                                                                                                                                               FEATURE:
NAME/KEY: MISC_PEATURE
LOCATION: (48)..(48).
OTHER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
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NAMENTY:
LOCATION: (51) (51)
OTHER INFORMATION: X IS ANY AMINO ACID OR NONEXISTENT
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Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 10; Conservative 0; Mismatches 0
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US-09-819-136-5
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APPLICANT: Dennis, Elizabeth S.
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Dennis, Elizabeth S.
APPLICANT: Dennis, Elizabeth S.
APPLICANT: Dennis, Elizabeth S.
APPLICANT: Lounow, Anna M.G.
APPLICANT: William J.
ITILE OF INVENTION: Method for inducing seed development by down-regulating
APPLICANT: Peacock, William J.
ITILE OF INVENTION: expression of the FIS2 gene
FILE REPERBNCE: 72-98A
CURRENT APPLICATION NUMBER: US/10/231,778
FILE REPERBNCE: 1999-09-20
FRIOR APPLICATION NUMBER: 60/101,184
PRIOR FILING DATE: 1998-09-21
PRIOR FILING DATE: 1998-09-21
PRIOR FILING DATE: 1998-09-22
                                                                                      GAPLICANT: Bilodeau, Pierre
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chauchory, Anna M.G.
APPLICANT: Churnow, Anna M.G.
APPLICANT: Luo, Ming
APPLICANT: Feacock, William J.
TITLE OF INVENTION: Method for inducing seed development by down-regulating
TITLE OF INVENTION: Method for inducing seed development by down-regulating
TITLE OF INVENTION: Method for inducing seed development by down-regulating
TITLE OF INVENTION: Method for inducing seed development by down-regulating
TITLE OF INVENTION: Method for inducing seed development by down-regulating
TITLE OF INVENTION: Method for inducing seed development by down-regulating
TITLE OF INVENTION: MOMBER: 09/1988.237
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1999-07-01
PRIOR 
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100.0%; Score 26; DB 14; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 10; Conservative 0; Mismatches 0; Indels
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1 LOCATION: (33)
2 OTHER INFORMATION: X at positions 1 to 63 is any amino acid
US-10-231-778-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-231-778-98

Sequence 98, Application US/10231778

Publication No. US20030126647A1

GENERAL INFORMATION:
APPLICANT: Bilodeau, Pierre
APPLICANT: Dennis, Elizabeth S.
APPLICANT: Koltunow, Anna M.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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Sequence 58, Application US/10231778
Publication No. US20030126647A1
GENERAL INFORMATION:
APPLICANT: Blodeau, Fierre
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Anna M.G.
APPLICANT: Chaudhury, Anna M.G.
APPLICANT: Luo, Ming
APPLICANT: Deacoré, William J. 178
CURRENT FILING DATE: 2002-11-08
FRIOR PELING DATE: 1990-09-2
PRIOR PELICATION NUMBER: 06/101,184
PRIOR APPLICATION NUMBER: AU PP6061
PRIOR APPLICATION NUMBER: AU PP6061
PRIOR APPLICATION NUMBER: AU PP6062
PRIOR APPLICATION NUMBER: AU PP6063
PRIOR APPLICATION NUMBER: AU PP6063
PRIOR PILING DATE: 1998-09-22
PRIOR PILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: AU PQ1346
PRIOR APPLICATION NUMBER: AU PO0345
PRIOR APPLICATION NUMBER: AU PO0346
PRIOR AU PO03404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: VARIANT
1 LOCATION: (1)..(63)
2 OTHER INFORMATION: X at positions 1 to 63 is any amino acid.
US-10-231-778-58
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 26; DB 9; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 10; Conservative 0; Mismatches 0; Indels
                                      NAME/KEY: VARIANT
COCATION: (28)
OTHER INFORMATION: Xaa = any amino acid or is not present
NAME/KEY: VARIANT
COCATION: (31)...(54)
OCHER INFORMATION: Xaa = any amino acid
US-09-819-136-5
OTHER INFORMATION: Xaa = any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CXXXXXXXX 10
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RESULT 95 US-10-231-778-78

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APPLICANT: Bilodeau, Pierre
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Anna M.G.
APPLICANT: Coltunow, Anna M.G.
APPLICANT: Luo, Ming
APPLICANT: Luo, Ming
APPLICANT: Pascock, William J.
TITLE OF INVENTION: Method for inducing seed development by down-regulating
TITLE OF INVENTION: Method for inducing seed development by down-regulating
TITLE OF INVENTION: MARINER: US/10/231,778
FILE REPERENCE: 72-98
FILE OF INVENTION NUMBER: 00/101,184
PRIOR FILING DATE: 1999-09-20
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: AU PP6061
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-01
PRIOR FILING DATE: 1999-07-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Motif
                                                                 Query Match 100.0%; Score 26; DB 14; Length 64; Best Local Similarity 100.0%; Pred. No. 0.6; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) LOCATION: (1)..(64)
; OTHER INFORMATION: X at positions 1 to 64 is any amino acid. US-10-231-778-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3-78-83
US-10-231-78-83
Sequence 83, Application US/10231778
Publication No. US20030126647A1
GENERAL INFORMATION:
APPLICANT: Bilodeau, Pierre
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Dennis, Elizabeth S.
APPLICANT: Koltunow, Anna M.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 68, Application US/10231778 Publication No. US20030126647A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CXXXXXXXX 10
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Best Local Similarity
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US-10-231-778-63
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APPLICANT: Bilodeau, Pierre
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chauna: Filiazbeth S.
APPLICANT: Columow, Anna M.G.
APPLICANT: Luo, Ming
APPLICANT: Eacock, William J.
TITLE OF INVENTION: Method for inducing seed development by down-regulating
TITLE OF INVENTION: Method for inducing seed development by down-regulating
TITLE OF INVENTION: MABER: US/10/231,778
TITLE OF INVENTION: MABER: US/10/231,778
TITLE OF INVENTION WINBER: US/10/231,778
CURRENT FILING DATE: 1999-09-21
PRIOR APPLICATION WINBER: 60/101,184
PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION WINBER: AU PP6061
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1999-07-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: VARIANT
LOCATION: (1)..(64)
OTHER INFORMATION: X at positions 1 to 64 is any amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: VARIANT

) LOCATION: (63)

) CTHEN INFORMATION: X at positions 1 to 63 is any amino acid.

US-10-231-778-98
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        PRIOR APPLICATION UNMBER: AU PEGGS
PRIOR APPLICATION NUMBER: 40 PEGGS
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-07-01
PRIOR PELLING DATE: 1999-07-01
PRIOR PRILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 239
SOFWRARE: PALENTIN VEY: 2.0
SEQ ID NO 98
LENGTH: 63
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Publication No. US20030126647A1
GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: AU PP6062
PRIOR FILING DATE: 1998-09-22
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ORGANISM: Artificial Sequence
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Query Match
Best Local Similarity 100.0%; Score 26; DB 14; Length 64;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 10; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
      PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 88
LENGTH: 64
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Sequence 68 Application US/10231778
Publication No. US20030126647A1
GENERAL INFORMATION:
APPLICANT: Bilodeau, Pierre
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Luo, Ming Miliam M.G.
APPLICANT: Luo, Ming William M.G.
APPLICANT: NOWBER: US/10/231,778
CURRENT FILING DATE: 1939-09-20
PRIOR PELING DATE: 1939-09-20
PRIOR APPLICATION NUMBER: AU PP6061
PRIOR APPLICATION NUMBER: AU PP6061
PRIOR PLING DATE: 1938-09-22
PRIOR FILING DATE: 1938-09-22
PRIOR FILING DATE: 1938-09-22
PRIOR PLING DATE: 1939-07-01
PRIOR APPLICATION NUMBER: AU PQ1345
PRIOR APPLICATION NUMBER: AU PQ1345
APPLICANT: Luo, Ming
APPLICANT: Luo, Ming
APPLICANT: Peacock, William J.
TITLE OF INVENTION: Method for inducing seed development by down-regulating
TITLE OF INVENTION: expression of the FIS2 gene
FILE REFERENCE: 72-98A
CURRENT APPLICATION NUMBER: US/10/231,778
CURRENT APPLICATION NUMBER: 09/398,237
PRIOR FILING DATE: 1999-09-20
PRIOR PLING DATE: 1999-09-21
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-22
PRIOR PLING DATE: 1999-07-01
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Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: VARIANT

1 LOCATION: (1). (64)

1 OTHER INFORMATION: X at positions 1 to 64 is any amino acid.

US-10-231-778-83
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ORGANISM: Artificial Sequence
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APPLICANT: Blicaeau, Pierre
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Columow, Anna M.G.
APPLICANT: Kollumow, Anna M.G.
APPLICANT: Luo, Ming
TITLE OF INVENTION: expression of the Fis2 gene
TITLE OF INVENTION: expression of the Fis2 gene
TITLE OF INVENTION: expression of the Fis2 gene
TITLE OF INVENTION: MADER: 1090-02-11-08
FILE REFERENCE: 72-98A
CURRENT PELING DATE: 1999-09-20
FRICR FILING DATE: 1999-09-20
FRICR FILING DATE: 1998-09-21
FRICR FILING DATE: 1998-09-22
FRICR FILING DATE: 1999-07-01
FRICR FILING 
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FEATURE:
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Motif FEATURE:
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LOCATION: (1)...(64)
COTHER INFORMATION: X at positions 1 to 64 is any amino acid.
US-10-231-778-103
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100.0%; Score 26; DB 14; Length 64;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                            NAME/KEY: VARIANT
1 LOCATION: (1)...(64)
2 OTHER INFORMATION: X at positions 1 to 64 is any amino acid.
US-10-231.778-88
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Publication No. US20030126647A1
APPLICANT: Bilodeau, Pierre
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Gaps

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US-10-231-778-93

Sequence 93, Application US/10231778

Publication No. U620030126647A1

GENERAL INFORMATION:
APPLICANT: Bilodeau, Pierre
APPLICANT: Bilodeau, Pierre
APPLICANT: Bilodeau, Pierre
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Channay, Anna M.G.
APPLICANT: Luo, Ming anna M.G.
APPLICANT: Koltunow, Anna M.G.
APPLICANT: Eascock, William M.G.
APPLICANT: William M.G.
APPLICANT: Walliam W.G.
APPLICANT: Peacock, William W.G.
APPLICANT: Peacock, William W.G.
APPLICANT: Worker of the FIS2 gene
TITLE OF INVENTION: Method for inducing seed development by down-regulating
TITLE OF INVENTION: Method for inducing seed development by GURENT APPLICANTON WHBER: US/10/231,778

CURRENT APPLICANTON NUMBER: 00/101,184

PRIOR APPLICATION NUMBER: AU PP6061

PRIOR APPLICATION NUMBER: AU PP6061

PRIOR APPLICATION NUMBER: AU PP6061

PRIOR APPLICATION NUMBER: AU PP6063

PRIOR APPLICATION NUMBER: AU PP6063

PRIOR APPLICATION NUMBER: AU PQ1346

PRIOR PILING DATE: 1999-07-01

PRIOR PILING DATE: 1999-07-01

PRIOR PILING DATE: 1999-07-01

PRIOR PILING DATE: 1999-07-01

PRIOR APPLICATION NUMBER: AU PQ1346

PRIOR APPLICATION NUMB
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1 LOCATION: (1)...(65)

1 OTHER INFORMATION: X at positions 1 to 65 is any amino acid.

US-10-231-778-73
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                                                                           PRIOR APPLICATION NUMBER: 60/101,184
PRIOR FILING DATE: 1998-09-21
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: AU PP6662
PRIOR APPLICATION NUMBER: AU PP6662
PRIOR PILING DATE: 1998-09-22
PRIOR PRIOR DATE: 1998-09-22
PRIOR PRIOR DATE: 1998-09-22
PRIOR PRIOR DATE: 1999-07-01
PRIOR PRIING DATE: 1999-07-01
PRIOR PILING DATE: 1999-07-01
PRIOR PILING DATE: 1999-07-01
PRIOR FILING DATE: 1
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ORGANISM: Artificial Seguence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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US-10-231-778-93
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Sequence 108, Application US/10231778

Publication No. US20030126647A1

GENERAL INPORMATION:

APPLICANT: Bilodeau, Fierre

APPLICANT: Chaudhury, Abdul M.

APPLICANT: Chowney, Mana M.G.

APPLICANT: Rolling M. Chaude Gor inducing seed development by down-regulating TILLE OF INVENTION: expression of the FIS2 gene

TITLE OF INVENTION: expression of the FIS2 gene

TITLE OF INVENTION: expression of the FIS2 gene

TITLE OF INVENTION: expression of the FIS2 gene

CURRENT FILING DATE: 2002-11-08

FRIOR FILING DATE: 1999-09-21

PRIOR PELING DATE: 1998-09-22

PRIOR PELING DATE: 1998-07-01

PRIOR PELING DATE: 1998-07-01

PRIOR PELING DATE: 1999-07-01

PRIOR PELING DATE: 1999-07-01
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APPLICANT: Bilodeau, Pierre
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chaudhury, Abdul M.
APPLICANT: Chunow, Anna M.G.
APPLICANT: Luo, Ming
APPLICANT: Luo, Ming
APPLICANT: Luo, Ming
APPLICANT: Luo, Ming
APPLICANT: Lao, Ming
APPLICANT: Corression of the FIS2 gene
CURRENT APPLICATION NUMBER: US/10/231,778
CURRENT APPLICATION ADDER: 2002-11-08
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CCATION: (1)..(64)
COTHER INFORMATION: X at positions 1 to 64 is any amino acid.
US-10-231-778-108
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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1 CXXXXXXXXC 10
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RESULT 107
US-09-952-559-1
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APPLICANT: Chaudhury, Abdul M.
APPLICANT: Low, Ming
APPLICANT: Low, Ming
APPLICANT: Low, Ming
APPLICANT: Low Number: Uson of the Fis2 gene
FITLE OF INVENTION: Method for inducing seed development by down-regulating
FITLE OF INVENTION: Method for inducing seed development by down-regulating
FITLE OF INVENTION: Method for inducing seed development by down-regulating
FITLE OF INVENTION: MADER: Uson 10-20
FITLE PEPERENCE: 129-84
CURRENT APPLICATION NUMBER: Uson 10-20
FRICK FILING DATE: 1998-09-22
FRICK FILING DATE: 1998-07-01
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Motif
FEATURE:
NAME/KEY: VARIANT
LOCATION:
COTHER INFORMATION: X at positions 1 to 65 is any amino acid.
US-10-231-778-93
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100.0%; Score 26; DB 14; Length 65;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 26; DB 14; Length 65; Best Local Similarity 100.0%; Pred. No. 0.6; Matches 10; Conservative 0; Mismatches 0; Indels
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1 LOCATION: (1)..(65)
2 OTHER INFORMATION: X at positions 1 to 65 is any amino acid
US-10-231-778-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 106
US-09-792-200B-20
; Sequence 20, Application US/09792200B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5-10-231-778-113
Sequence 113, Application US/10231778
Sublication No. US20030126647A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bilodeau, Pierre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CXXXXXXXX 10
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APPLICANT: Gage, Frederick H.
Subr. Steven T.
TITLE OF INVENTION: Modified Lepidopteran Receptors
and Hybrid Multi-Functional Proteins for Use in Transcr:
and Transgene Expression Regulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHER INFORMATION: Consensus disintegrin domain
NAME/KEY: MISC_FEATURE
LOCATION: (5)..(9)
CHER INFORMATION: Xaa is 3-5 varying residues in a consensus sequence
NAME/KEY: MISC_FEATURE
LOCATION: (11)..(16)
CHER INFORMATION: Xaa is 3-6 varying residues in a consensus sequence
NAME/KEY: MISC_FEATURE
LOCATION: (19)..(22)
CHER INFORMATION: Xaa is 2-4 varying residues in a consensus sequence
NAME/KEY: MISC_FEATURE
LOCATION: (19)..(30)
CHER INFORMATION: Xaa is 7 varying residues in a consensus sequence
NAME/KEY: MISC_FEATURE
LOCATION: (32)..(37)
CHER INFORMATION: Xaa is 4-6 varying residues in a consensus sequence
NAME/KEY: MISC_FEATURE
LOCATION: (40)..(43)
CHER INFORMATION: Xaa is 2-4 varying residues in a consensus sequence
NAME/KEY: MISC_FEATURE
LOCATION: (45)..(53)
CHER INFORMATION: Xaa is 8 varying residues in a consensus sequence
NAME/KEY: MISC_FEATURE
LOCATION: (45)..(52)
CTHER INFORMATION: Xaa is 8 varying residues in a consensus sequence
NAME/KEY: MISC_FEATURE
LOCATION: (45)..(50)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (54)...(60)
COTHER INFORMATION: Xaa is 5-7 varying residues in a consensus sequence NAME/KEY: MISC FEATURE
LOCATION: (62)...(66)
COTHER INFORMATION: Xaa is 3-5 varying residues in a consensus sequence US-09-792-2008-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
GENERAL INFORMATION

APPLICANT: Fanslow, William C.
APPLICANT: Fanslow, William C.
APPLICANT: Fondexer, Kult
APPLICANT: Cerretti, Douglas P.
APPLICANT: Black, Roy A.
TITLE REPERENCE: 2058-A
CURRENT APPLICATION NUMBER: US/09/792,200B
CURRENT FILING DATE: 2001-02-25
FRIOR FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3:1
SEQ ID NO 20
LENGTH: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09952559 Patent No. US20020048815A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 10; Conservative
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RESULT 109
US-09-949-278-1
| Sequence 1, Application US/09949278
| Sequence 1, Application US/09949278
| Publication No. US2020187972A1
| GENERAL INFORMATION:
| APPLICANT: EVANS, Ronald
| APPLICANT: EVANS, ENTIQUE
| TITLE OF INVENTION: EXOGENOUS
| TITLE OF INVENTION GENES IN MANMALIAN SYSTEMS, AND PRODUCTS RELATED THERETO
| TITLE REFERENCE: SALK2310
| CURRENT APPLICATION NUMBER: US/09/949,278
| CURRENT APPLICATION NUMBER: 09/079,570
| PRIOR FILING DATE: 1998-05-14
| NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9; Length 71;
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Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (53)..(54)
OTHER INFORMATION: Amny amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) LOCATION: (67)...(69)
) OTHER INFORMATION: Any amino acid
US-09-042-488B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MOD RES
LOCATION: (40)...(47)
OTHER INFORMATION: Any amino acid
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LOCATION: (56)..(57)
OTHER INFORMATION: Any amino acid
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OTHER INFORMATION: Any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MOD RES
COCATION: (59)...(60)
OTHER INFORMATION: Any amino acid
NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (63)..(64)
OTHER INFORMATION: Any amino acid
                                                                                                                                                                                                                        OTHER INFORMATION: Any amino acid MAME/KEY: MOD RES LOCATION: (1407)...(17) OTHER INFORMATION: Any amino acid other information: Any amino acid
                                                                                                                                                                                                                                                                                                                            NAME/KEY: MOD RES
CHCRATION: (19)...(20)
CHCRATION: Any amino acid
NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (23)
OTHER INFORMATION: Any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MOD RES
LOCATION: (26)
OTHER INFORMATION: Any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MOD RES
LOCATION: (28)...(38)
OTHER INFORMATION: Any amino acid
OTHER INFORMATION: Any amino acid
NAME/KEY: MOD_RES
                                                                                                                         LOCATION: (10)
OTHER INFORMATION: Any amino acid
                                                                         OTHER INFORMATION: Any amino acid
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LOCATION: (53)..(
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                                                                                                                                                                          NAME/KEY: MOD RES
LOCATION: (12)
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LOCATION: (49)..(
                                                                                                    NAME/KEY: MOD RES
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; Sequence 1, Application US/09042486B
; Patent No. US20020177564A1
; General Information:
    APPLICANT: BYONLD M.
    APPLICANTON: MAMMALIAN SYSTEMS, AND PRODUCTS REALTED THERETO
    TITLE OF INVENTION: MAMMALE: 1909-0.2
    CURRENT PELING DATE: 1998-0.3-16
    PRIOR PILING DATE: 1996-0.3-16
    PRIOR PILING DATE: 1996-0.4-05
    NUMBER OF SEQ ID NOS: 18
    SOFTWARE: PALENTIN VAINES: 08/628,830
    SOFTWARE: PALENTIN VAINES: DELING DATE: 1996-0.4-05
    NUMBER OF SEQ ID NOS: 18
    SEQ ID NO 1
    LENGTH: 71
    LENGTH: 71
    LENGTH: 71
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                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: TRANSMILLE
COMPUTER: PASTENCY DOS
SOFTWARE: FASTENCY DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/952,559
FILING DATE: 13-Sep-2001
CLASSIFICATION: CURROWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Consensus
OTHER INFORMATION: peptide sequence
NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/891,298
FILING DATE: UNKnown-
ATTORNEY/ABGNT INFORMATION:

NAME: Reiter, Stephen E
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: 4Uknown-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1469
TELEFAX: 619-677-1465
TELEPHONE: 619-677-1465
TELEPHONE: 619-677-1465
TELEPHONE: 71 amino acide
LENGTH: 71 amino acide
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US-09-952-559-1
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OTHER INFORMATION: Any amino acid
NAME/KEY: MOD RES
LOCATION: (5)...(6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 10; Conservative
CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CXXXXXXX 10
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                                                      USA
                        STATE: CA
COUNTRY: US
ZIP: 92121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -09-042-488B-1
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Gaps

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NAME/KEY: MOD_RES
LOCATION: (8)
OTHER INFORMATION: any au
FEATURE:
                                                       1 CXXXXXXX 10
                                                                                              39 CXXXXXXXX 48
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LOCATION: (14)..(17)
OTHER INFORMATION: any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: MOD_RES
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Forman, Barry M.
Indesono, Kazuhiko
TITLE OF INVENTION: ALLOSTERIC CONTROL OF NUCLEAR HORMONE RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEB: Gray Cary Ware & Freidenrich
STEEDT: 4365 Executive Drive, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASESE for Windows DEMONSTRATION Version 2.0D

CURRENT APPLICATION NUMBER: US/10/236,745

FILING DATE: 06-Sep-2002

CLASSIFICATION: <UNKNOWN>
                                                         TYPE: PRT
CRGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Binding domain of the steroid/thyroid hormone
OTHER INFORMATION: receptor
NAME/KEY: VARIANT
COTHER INFORMATION: receptor
NAME/KEY: VARIANT
COCATION: (1)..(71)
COTHER INFORMATION: Xaa is any amino acid
US-09-949-278-1
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                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 26; DB 9; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: SALK 1450-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/877,966B
FILING DATE: 17-70N-1997
APPLICATION NUMBER: 08/72,217
FILING DATE: 13-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/10236745; Publication No. US20030083469A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 619-677-1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 71 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 619-677-1465
TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
SOFTWARE: PatentIn version 3.0 SEQ ID NO 1 LENGTH: 71
                                                                                                                                                                                                                                                                                                                                                                                                             1 CXXXXXXX 10
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US-10-236-745-1
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Past Local Similarity 100.04; Pred No. 0.62; O; Indels O; Gaps O; Maches 10; Constrainty 100.04; Pred No. 0.62; O; Indels O; Gaps O; Sethers 10; Constraints O; Mismatches O; Mismatches
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INFORMATION: any amino acid

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Sequence 247931, Application US/10424599
| Sequence 247931, Application US/10424599
| Publication No. US20040031072A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: La Rosa Thomas J
| APPLICANT: Zhou Yihua
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| TITLE OF INVENTION NUMBER: US/10/424,599
| CURRENT APPLICATION NUMBER: US/10/424,599
| NUMBER OF SEQ ID NOS: 285684
| SEQ ID NO 247331
| LEMIGTH: 95
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100.0%; Pred. No. 0.67;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 26; DB 15; Length 71; 100.0%; Pred. No. 0.62; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_65912C.1.pep
US-10-424-599-247931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(95)
OTHER INFORMATION: unsure at all Xaa locations
APPLICATION NOMBER: US 09/17,917, PILING DATE: 07-UNN-1995
APPLICATION NUMBER: US 08/244,857
FILING DATE: 14-UNN-1994
APPLICATION NUMBER: WO 93/11755
FILING DATE: 18-DEC-1992
APPLICATION NUMBER: US 07/809,980
FILING DATE: 18-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: 941,9979
                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown
MOLECULE TYPE: procein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEBHONE: 619-546-1995
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 71 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 114
US-10-011-859-23
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Publication No. US20040006144A1
GENERAL INFORMATION:
APPLICANT: Evans, Ronald M.
Heyman, Richard A.
Boehm, Marcus F.
Eichele, Gregor
Thaller, Christina
Thaller, Christina
MEDIATED BY RETINOID RECEPTORS AND COMPOUNDS USEFUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STRRET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: UGA
COUNTRY: BOOTI
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IDP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/458,880
FILING DATE: 10-Jun-2003
CLASSIFICATION 1424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 26; DB 14; Length 71; ilarity 100.0%; Pred. No. 0.62; Conservative 0; Mismatches 0; Indels
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APPLICATION NUMBER: US/09/350,648
                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: MOD RES
LOCATION: (597..(60)
OTHER INFORMATION: any amino acid
FEATURE:
NAME/KEY: MOD RES
LOCATION: (637..(64)
OTHER INFORMATION: any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:

NAME/KEY: MOD RES

LOCATION: (67)...(69)

OTHER INFORMATION: any amino acid
US-10-302-557-33
                                                                                                                                                                          FEATURE:

NAME/KEY: MOD RES

LOCATION: (53)...(54)

OTHER INFORMATION: any amino acid
                                                                                                      NAME/KEY: MOD_RES
LOCATION: (49)..(51)
OTHER INFORMATION: any amino acid
                                   LOCATION: (40)..(47)
OTHER INFORMATION: any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CXXXXXXXC 48
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                                                                                                                                                                                                                                                                                           NAME/KEY: MOD RES
LOCATION: (56)..(57)
OTHER INFORMATION: any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 10; Conserv
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US-10-458-880-1
                                                                                                                                                                                                                                                                         FEATURE:
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APPLICANT: Sum, ...
Chinis, Chetan
Miller, Louis H.
Peterson, David S.
Su, Xin - Zhaun
Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/10/153,273
FILING DATE: 21-May-2002
CLASSIFICATION: _<Unknown>
                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: FULLET, MICHAEL
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELECOMMULICATION INFORMATION:
TELEPHONE: (619) 235-6850
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-153-273-14
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SEQUENCE CHARACTERISTICS:
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                             Sequence 14, Application US/10153273
Publication No. US2020169305A1
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
                                                                                                                                                         Kim L.
nis, Chetan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE: internal
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US-10-153-273-21
                                                                3-273-14
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Sequence 23, Application US/10011859; publication No. US20020147328A1; GENERAL INFORMATION:
APPLICANT: Shappard, Paul O.
APPLICANT: Shappard, Paul O.
APPLICANT: Shappard, Stephen R.
ITILE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR HOMOLOGS
FILE REFERENCE: 97-75
CURRENT APPLICATION NUMBER: US/10/011,859
CURRENT APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US/09/253,316
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-19
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 34
SOFTWAREE: FASEURE FILING DATE: 1998-02-20
SOFTWAREE: FASEURE FILING DATE: 1998-102-20
LENGTH: 127
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CRGANISM:
FEATURE:
OTHER INFORMATION: connective tissue growth factor family motif
NAME/KEY: VARIANT
LOCATION: (2)...(9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 26; DB 13; Length 127; larity 100.0%; Pred. No. 0.73; Conservative 0; Mismatches n. Indol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (62)

OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: VARIANT

LOCATION: (63)...(63)

OTHER INFORMATION: Xaa is any amino acid or not present

NAME/KEY: VARIANT

LOCATION: (63)...(106)

OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (107)...(108)
OTHER INFORMATION: Xaa is any amino acid or not present
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (123)...(126)
; OTHER INFORMATION: Xaa is any amino acid or not present
US-10-011-859-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (2)...(9)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: VARIANT
LOCATION: (10)...(11)
OTHER INFORMATION: Xaa is any amino acid or not present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: VARIANT
LOCATION: (32)...(32)
OTHER INFORMATION: Xaa is any amino acid or not present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: VARIANT
LOCATION: (39)...(40)
OTHER INFORMATION: Xaa is any amino acid or not present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: VARIANT
LOCATION: (54).
OTHER INFORMATION: Xaa is any amino acid or not present
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (110)...(122)
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT
LOCATION: (13)...(31)
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: VARIANT
LOCATION: (34)...(38)
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (42)...(53)
DTHER INFORMATION: Xaa is any amino acid
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Best Local Similarity
Matches 10; Conserv
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Query Match
100.0%; Score 26; DB 13; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 10; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                  Sequence 21, Application US/10153273
Publication No. US2020169305A1
GENERAL INFORMATION:
APPLICANT: Sim. Kim L.
APPLICANT: Sim. Kim L.
Miller, Louis H.
Peterson, David S.
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Search completed: May 4, 2004, 07:18:34 Job time : 43 secs
  COUNTRY: US
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APPLICANT: Sim, Kim L.
Chitnis, Chetan
Miler, Louis H.
Peterson, David S.
Su, Xin-zham
Nellems, Thomas B.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM BRYTHROCYTE BINDING PROTEINS
Su, xin-zhaun Wellems, Thomas E. TITLE OF INVENTION: BINDING PROTEINS AND PLASMODIUM VIVAX AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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100.0%; Score 26; DB 13; Length 311;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 10; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                            COMPUTER READBELE FORM:

EDGINATION TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE: 21-May-2002
CLASSIFICATION: -Unknown>
APPLICATION NUMBER: US/09/210,288
FILING DATE: -Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: PLULer, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/COCKET NUMBER: 36,516
REFERENCE/COCKET NUMBER: 18,50,516
REFERENCE/COCKET NUMBER: 18,50,516
RELEPHONE: (619) 235-0176
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE: internal ORIGINAL SOURCE: SEQUENCE DESCRIPTION: SEQ ID NO: 21: US-10-153-273-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 311 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17, Application US/10153273 Publication No. US20020169305A1
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STATE: California
                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 CXXXXXXXX 237
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                                                                                                                                                                                                                                            COUNTRY: US
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US-10-153-273-17
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COMPUTER READMELE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION NAMER: US/10/153,273
FILING DATE: 21-MAY-2002
CLASSIFICATION DATA:
APPLICATION NAMER: US/09/210,288
FILING DATE: CUNKnown>
ATTORNEY/AGENT INFORMATION:
NAME: FULLE: Michael
REGISTRATICN NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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100.0%; Score 26; DB 13;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 10; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

SEQUENCE DESCRIPTION: SEQ ID NO: 17:

US-10-153-273-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 324 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 CXXXXXXXX 320
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249, App 2299, A
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Sequence
Sequence
US-09-249-472-299
US-09-249-472-299
US-09-249-472-299
US-09-249-472-299
US-09-249-472-299
US-09-249-471-229
US-09-249-451-200
US-09-249-451-299
US-09-249-451-299
US-08-809-455-299
US-08-809-455-299
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US-08-809-455-299
US-08-809-455-299
US-08-809-456-299
US-08-808-866-399-272
US-08-808-399-173
US-08-486-399-173
US-08-486-399-173
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/cgm2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgm2_6/ptodata/2/iaa/BECOMB.pep:*
/cgm2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgm2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgm2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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Maximum Match 100%
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Maximum I
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Query Match 65.4%; Score 17; DB 2; Length 10; Best Local Similarity 100.0%; Pred. No. 7e+02; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: Xaa in locations 2 to 10 is an ) OTHER INFORMATION: amino acid. US-08-465-380-200
                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: 3.00rage
COMPUTER: IEM Compatible
COMPUTER: IEM Compatible
OPERATING SYSTEM: IEM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/08/465,380
FILING DATE: Une 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: 08/326,110
FILING DATE: OCTOBE 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE I.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/268
TELECOMMUNICATION INFORMATION:
TELEFAX: (213) 955-0440
TELEFAX: (7-3510
TELEFAX: 67-3510
TELEFAX: 67-3510
TELEFAX: 10 AMINO ACIGS
SEQUENCE: NAME OCIGS
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FRAGMENT TYPE: internal fragment
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XGY: linear
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                                                                                                                                                                                                                                                   Sequence 39, Application US/08526710

Patent No. 5622699

GENERAL INFORMATION:

APPLICANT: Pasqualini, Erkki

APPLICANT: Pasqualini, Renata

TITLE OF INVENTION: Method of Identifying Molecules That

TITLE OF INVENTION: Home to a Selected Organ in Vivo

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: CAMDRESSEE: CAMDRESSEE:

CAMPANDENCE ADDRESSEE: CAMDRESSEE: CAMD
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Patent No. 5863894

GENTRAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: Yves R. Laroche, Laurent S. Jespers, APPLICANT: Yanik G.J. Gansemans, Matthew Moyle, APPLICANT: Patrick G.J. Gansemans, Matthew Moyle, APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEWATODE-EXTRACTED ANTICOAGULANT: TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSED: Lyon & Lyon
CORRESSED: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Diego
SIATE: Callfornia
CUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM FC COMPATIBLE
OMFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,710
FILING DATE: 11-SEP-1995
CLASIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 65.4%; Score 17; DB 1;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 9; Conservative 0; Mismatches (
                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 amino acids
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US-08-465-380-200
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GOTIS H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yoes R. Laroche, Laurent S. Jespers,
APPLICANT: Yes R. Laroche, Laurent S. Jespers,
APPLICANT: Yes R. Laroche, Laurent S. Jespers,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 90071
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
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COMPUTER: IEM COMPATIBLE
OPERATING SYSTEM: IEM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,380
Sequence 249, Application US/08465380
Patent No. 5863894
                                                                                                                                                                                                                                                                                                                                  E: Lyon & Lyon
633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                             STREET: 633 West Fi
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                Suite 4700
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STREET: Gay West Fifth Street STREET: 633 West Fifth Street CITY: Los har

0; Gaps

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Query Match
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                      OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 5.5" Diskette, 1.6"
COMPUTER: 18M Compatible
COMPUTER: 18M Compatible
SOFTWARE: Word Perfect 5.1
CURREMY APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT THORMATION:
NAME: BIGGS, SUZAMNE L.
REGISTRATION NUMBER: 30,158
REFRERENCE/DOCKET NUMBER: 30,158
REFRERENCE/DOCKET NUMBER: 30,158
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               internal fragment
                                                                                                        TYPE: amino acid
TOPOLOGY: linear
FRAGMENT TYPE: internal fragment
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-310
INFORMATION FOR SEQ ID NO: 352:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
    (213) 955-0440
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERESTICS:
LENGTH: 10 amino acids
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OTHER INFORMATION:
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US-08-465-380-352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 299, Application US/08465380

Patent No. 5863894

GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys, APPLICANT: Yeas R. Laroche, Laurent S. Jespers, APPLICANT: Yannick G.J. Gansemans, Matthew Moyle, APPLICANT: Peter W. Bergum; TITLE OF INVENTION: NEWATODE-EXTRACTED ANTICOAGULANT: TITLE OF INVENTION: REPOTEIN
NUMBER OF SEQUENCES: 356

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

65.4%; Score 17; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: ENCOMPATION:
COMPUTER: IBM COMPATION:
COMPUTER: IBM COMPATION:
COMPUTER: IBM COMPATION:
COMPUTER: MORE PETFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,380
FILING DATE: June 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY AGENT INPORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/POCKET NUMBER: 30,158
REFERENCE/POCKET NUMBER: 31,268
TELECOMMUNICATION INPERATION:
TELEDHONE: (213) 489-1600
  FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY AGENT INFORMATION:
NAME: BIGGS, SUZANUE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPA: (7-3510
INFORMATION FOR SEQ ID NO: 249:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acide
TYPE: amino acide
                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CXXXXXXXX 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CXXXXXXX 9
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                                      Sequence 249, Application US/08486397

Sequence 249, Application US/08486397

Sequence 249, Application US/08486397

Sequence 249, Application US/08486397

APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys, APPLICANT: Yves R. Larcoche, Laurent S. Jespers, APPLICANT: Peter W. Bergum

TILE OF INVENTION: PROTEIN

TILE OF INVENTION: PROTEIN

TILE OF SEQUENCES: 357

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.4%; Score 17; DB 2; Length 10;
100.0%; Pred. No. 7e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: George P. Vlasuk, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Perer W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Xaa in locations 2 to 10 is an ; OTHER INFORWATION: amino acid. US-08-486-397-249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: SOCYAGE
COMPUTER: BM Compatible
OPERATIOS SYSTEM: BM P.C. DOS 5.0
SOFFWARE: WORD PETECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: JUNE 5, 1995
CLASSIFICATION NUMBER: US/08/486,397
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE 1.
REFERENCE/DOCKET NUMBER: 30,158
TELEPHONE: (213) 469-1600
TELEPA: 67-3510
TELEPA: 67-3510
TELEPA: 67-3510
TELEPA: 67-3510
TELEPA: 10 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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Patent No. 5866542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: internal fragment FEATURE:
                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CXXXXXXXX 9
                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
US-08-486-397-299
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65.4%; Score 17; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                 Length 10;
                                              Query Match 65.4%; Score 17; DB 2; Length 10; Best Local Similarity 100.0%; Pred. No. 7e+02; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yoss R. Laroche, Laurent S. Jespers,
APPLICANT: Yes R. Laroche, Laurent S. Jespers,
APPLICANT: Peter W. Bergum.
APPLICANT: Peter W. Bergum.
TITLE OF INVENTION: NEMATOBE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SECUENCES: 357
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Suite 4700
CITY: Los Angeles
STRTE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: BR Compatible
CORRATIOR SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRAIN APPLICATION DATA:
CURRAIN APPLICATION DATA:
APPLICATION NUMBER: US/08/486,397
TILING DATE: June 5, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: OCCOBER 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISSTRATION NUMBER: 30,158
REFERENCY/DOCKET NUMBER: 213/269
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                               Sequence 200, Application US/08486397; Patent No. 5866542; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 10 amino acids TYPE: amino acid
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US-08-465-380-352
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Gaps

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Query Match 65.4%; Score 17; DB 2; Length 10; Best Local Similarity 100.0%; Pred. No. 7e+02; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ); OTHER INFORMATION: Xaa in locations 2 to 10 is an CTHER INFORMATION: amino acid. US-08-486-397-352
        MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: atorage
COMPUTER: BM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,397
FILING DATE: Une 5,1995
CLASSIFICATION: 530
PRIOR APPLICATION 530
PRIOR APPLICATION DATA:
ATDING DATE: OCTOBER 19,1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 31,269
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 352:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CXXXXXXXX 9
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US-08-486-399-200
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Patent No. 586642

GENERAL INFORMATION:

APPLICANT: George P. Vlasuk, Patric H. Stanssens,

APPLICANT: Yves R. Laroche, Laurent S. Jespers,

APPLICANT: Yves R. Laroche, Laurent S. Jespers,

APPLICANT: Yansiok G.J. Gansemans, Matthew Moyle,

APPLICANT: Pannick G.J. Gansemans, Matthew Moyle,

APPLICANT: Peter W. Bergum

TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT;

TITLE OF INVENTION: PROTEIN

WUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

CHARLESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.4%; Score 17; DB 2; Length 10; 100.0%; Pred. No. 7e+02; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid. US-08-486-397-299
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 357
CARRESPONDERS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: Los Angeles
STATE: California
COMPTER: U.S.A.
ZIP: 90071
COMPTER: IBM COMPATIBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Groade
COMPUTER: IBM COMPATIBLE
OMPRATICALION DATA:
APPLICATION NUMBER: 1995
CLASIFICATION NUMBER: 08/326,110
FILING DATE: OCTOBER: 08/326,110
FILING DATE: OCTOBER: 08/326,110
FILING DATE: OCTOBER: 08/326,110
FILING DATE: OCTOBER: 30,158
ATSTERNICATION NUMBER: 30,158
REGISTRATION NUMBER: 30,158
REGISTRATION NUMBER: 30,158
REGISTRATION NUMBER: 30,158
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 30,158
REFERENCE/CALION SEGO ID NO: 299:
SEQUENCE CHARACTERISTICS:
FURNATHER 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
FRACMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Conservative
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Los Angeles
STATE: California
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Sequence 299, Application US/08486399 |
| Sequence 299, Application US/08486399 |
| Patent No. 586643 |
| Patent No. 586643 |
| GENERAL INFORMATION: |
| APPLICANT: Oris H.L. Mensens, Marc J. Lauwereys, APPLICANT: Yves R. Laroche, Laurent S. Jespers, APPLICANT: Yves R. Laroche, Laurent S. Jespers, APPLICANT: Patent W. Bergum |
| TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT |
| TITLE OF INVENTION: PROTEIN |
| NUMBER OF SEQUENCES: 356 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSE: Lyon & Lyon |
| STREET: 631464 4700 |
| STREET: 531464 4700 |
| STREET
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 65.4%; Score 17; DB 2; Length 10; Best Local Similarity 100.0%; Pred. No. 7e+02; Matches 9; Conservative 0; Mismatches 0; Indels
LENGTH: 10 amino acids
TYPE: amino acid
TYPE: anino acid
FRAGMENT TYPE: linear
FRAGMENT TYPE: internal fragment
FRATURE:
OTHER INFORMATION: Xaa in locations 2 to 10 is an
OTHER INFORMATION: amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid. US-08-486-399-299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: Btorage
COMPUTER: Btorage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DIATA:
APPLICATION NUMBER: US/08/466,399
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
ATTORNEY AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
ATTORNEY AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE DOCKET NUMBER: 213/270
RELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 488-1600
TELEFA: (213) 955-0440
TELER: (7-3510
INFORMATION FOR SEQ ID NO: 299:
EMOUTH: 10 anino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE; internal fragment FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CXXXXXXXX 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CXXXXXXX 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                               US-08-486-399-249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Jozis H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid. US-08-486-399-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 65.4%; Score 17; DB 2; Best Local Similarity 100.0%; Pred. No. 7e+02; Matches 9; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPESSEE: 1900 & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STRIET: California
COUNTRY: U.S.A.
ZIP: 90071
ZIP: 90071
ZIP: 90071
ZIP: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.0" Diskette, 1.44 Mb
MEDIUM DATE: DOCODET 18, 1994
ATTONNEY/AGENT INPORMATION:
MAME: BIGGS, SUZANNE L.
MEDIUM TREFERNCE/DOCKET NUMBER: 213/270
TELECOMUNICATION INPORMATION:
TELECOMUNICATION INDOM
TELECOMUNICATION INDOM
TELECOMUNICATION:
TELECO
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANB L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/270
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELEPHONE: (213) 955-040
ITELEX: 67-3510
INFORMATION FOR SEQ ID NO: 200: SEQUENCE CHARACTERISTICS: LENGTH: 10 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 249, Application US/08486399 Patent No. 5866543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXXXXXXXX 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CXXXXXXXX 9
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US-08-486-399-249
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TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 200:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 9; Conservative
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     Gaps
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0
                                                                                     KESULT 13
US-08-486-399-352
Sequence 352, Application US/08486399
Patent No. 5866543
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Parnick G.J. Gansemans, Matthew Moyle,
APPLICANT: Promick G.J. Gansemans, Matthew Moyle,
APPLICANT: Promick G.J. Gansemans, Matthew Moyle,
APPLICANT: PROMICE: 356
CORRESPONDENCE ADDRESSS:
ADDRESSES: 190n & Lyon
STREET: G.J. West Fifth Street
STREET: G.J. West Fifth Street
STREET: G.J. Google STATE: California
CONNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.4%; Score 17; DB 2; Length 10; 100.0%; Pred. No. 7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid. US-08-486-399-352
     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: SCOTSUS
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,399
FILING DATE: June 5, 1995
CLASSIFCATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: OCCODER 18, 1994
ATTORNEY/ACENT INFORMATION:
NAME: BIGGS, SUZANNE L.
RECISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/270
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 67-3510
TELEEX: 67-3510
TELEEX: 67-3510
TELEEX: 67-3510
SECTION FOR SEG DID NO: 352:
SECTION OF MERCENCE TRANSTICE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-461-965-200
; Sequence 200, Application US/08461965
; Patent No. 5872098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 9; Conservative
     9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 1
                                                      1 CXXXXXXXX 9
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          Matches
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UG-08-461-965-249

UG-08-461-965-249

; Sequence 249, Application US/08461965
; Patent No. 5872096
; GENERAL INFORMATION:
    APPLICANT: George P. Vlasuk, Patric H. Stanssens,
    APPLICANT: APPLICANT: APPLICANT: Yees R. Laroche, Laurent S. Jespers,
    APPLICANT: Yees R. Laroche, Laurent S. Jespers,
    APPLICANT: Yennick G.J. Gansemans, Matthew Moyle,
    APPLICANT: Peter W. Bergum
    TILLE OF INVENTION: PROTEIN
    TILLE OF INVENTION: PROTEIN
    NUMBER OF SEQUENCES: 356
    CORRESPONDENCES: 356
    ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.4%; Score 17; DB 2; Length 10; 100.0%; Pred. No. 7e+02; tive 0; Mismatches 0; Indels
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Joris H.L. Laroche, Laurent S. Jespers,
APPLICANT: Yees R. Laroche, Laurent S. Jespers,
APPLICANT: Yennick G.J. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Xaa in locations 2 to 10 is an ; OTHER INFORMATION: amino acid. US-08-461-965-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTY.

ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: ENCROPATION
COMPUTER: ENCROPATION
SOFTWARE: ENCY DATA:
APPLICATION NUMBER: US/08/461,965
FILING DATE: UNDER: 08/326,110
PRICR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
PILING DATE: OCCODET 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE:
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 30,243
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
                                                                                                                                                                                                                                                                                                          ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700 CITY: Los Angeles STATE: California COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
FRAGMENT TYPE: internal fragment
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Parent No. 5972098

Parent No. 5972098

Patent No. 5972098

APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: Yannick G.J. Gansemans, Matthew Moyle, APPLICANT: Yannick G.J. Gansemans, Matthew Moyle, APPLICANT: Peter W. Bergum

TITLE OF INVENTION: NEWATODE-EXTRACTED ANTICOAGULANT

TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES: 356

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Lifth Street
STREET: 631 West Lifth Street
STREET: Suite 4700

CITY: Los Angeles
STREET: Suite 4700

CITY: Los Angeles
STREET: Suite ATO
COUNTRY: U.S.A.

COMPUTER READALE FORM:
MEDIUM TYPE: Storage

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION NUMBER: US/08/461,965

FILING DATE: Unne 5, 1995

CLASSIFICATION NUMBER: 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.

REGISTRATION NUMBER: 30,158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query March 65.4%; Score 17; DB 2; Length 10; Best Local Similarity 100.0%; Pred. No. 7e+02; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid. US-08-461-965-299
    SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,965
FILING DATE: Unre 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE I.
REFERENCE/DOCKET NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 210/243
REFERENCE/DOCKET NUMBER: 210/243
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELERAX: (213) 955-0440
TELERAX: (213) 955-0440
TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 299:
SEQUENCE CHARACTERISTICS:
SEGUENCE CHARACTERISTICS:
SEGUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid.
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 134 Compatible
COMPUTER: TBM Compatible
OPPRATING SYSTEM: TBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,965
FILING DATE: US/08/461,965
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 210/243
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 249:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE AMINO acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
FRAGMENT TYPE: internal fragment
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CXXXXXXX 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CXXXXXXX 9
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US-08-461-965-299
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US-08-634-641-249

Sequence 249, Application US/08634641

Patent No. 5955294

GENERAL INCRNATION:

APPLICANT: Vlasuk, George P. Vlasuk

APPLICANT: Stanssens, Patrick Eric Hugo

APPLICANT: Lauwereys, Marc Josef

APPLICANT: Lauwereys, Marc Josef

APPLICANT: Lauwereys, Marc Josef

APPLICANT: Jasoche, Yves Rene

APPLICANT: Jasoche, Yves Rene

APPLICANT: Jasoche, Watchen

APPLICANT: Moyle, Matchew

APPLICANT: Moyle, Matchew

ITILE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT

TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT

TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT

TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT

STREET: 630 Weet Fifth Street

STREET: 630 Weet Fifth Street

STREET: GOORGESTONERS: 36

CITY: LOS ANGELDES

CITY: LOS ANGELDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 65.4%; Score 17; DB 2; Length 10; Best Local Similarity 100.0%; Pred. No. 7e+02; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage
COMPUTER: 1BM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,641
FILING DATE: April 19, 1996
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
                                                                                               219/136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE: internal fragment
                                                                               REFERENCE DOCKET NUMBER: 219/1
TELECOMUNICATION INFORMATION:
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEG ID NO: 200: SEQUENCE CHARACTERISTICS:
LENGTH: 10 anino acids
TYPE: amino acids
TOPOLOGY: linear
        NAME: BIGGS, SUZANNE L. REGISTRATION NUMBER: 30,158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CXXXXXXXX 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Vlasuk, George P. Vlasuk
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Bauweres, Marc Josef
APPLICANT: Lauweres, Marc Josef
APPLICANT: Lauweres, Marc Josef
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gansemns, Yannick Georges Jozef
APPLICANT: Bergum, Peter W.
APPLICANT: Bergum, Nemathow
APPLICANT: Bergum, Nemathobe-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid. US-08-461-965-352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTY: 0.5.A.

ZIE: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5." Diskette, 1.44 Mb
MEDIUM TYPE: 3.5." DISKette, 1.44
REFERENCE/DOCKET NUMBER: 210/243
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
INCRMATION FOR SEQ ID NO: 352:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 anino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/486,399
FILING DATE: June S, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June S, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June S, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June S, 1995
APPLICATION NUMBER: 08/41,965
FILING DATE: June S, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: June S, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: June S, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: June S, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE: internal fragment FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXXXXXXX 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CXXXXXXXX 9
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US-08-634-641-200
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) Sequence 352, Application US/08634641
) Patent No. 2955294
| GENERAL INFORMATION:
| APPLICANT: Vlasuk, George P. Vlasuk
| APPLICANT: Stansens, Patrick Eric Hugo
| APPLICANT: Laroche, Yves Rene
| APPLICANT: Laroche, Yves Rene
| APPLICANT: Gansemans, Yannick Georges Jozef
| CONRESSED: Lyon & Lyon
| STREET: Galfornia
| CONNEY: US.A.
| STREET: Galfornia
| CONNEY: US.A.
| CONPUTER: End Compatible
| COMPUTER: Mord Perfect 5.1
| CURRENT APPLICATION NUMBER: US/08/64,641
| FILING DATE: April 19, 1966
| PRICATION NUMBER: Galfornia
| APPLICATION NUMBER: Galfornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.4%; Score 17; DB 2; Length 10; 100.0%; Pred. No. 7e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid. US-08-634-641-299
                                                                                                                                                                                                                                   219/136
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: OCCODES 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUIZANNE L.
REGISTRACTION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 219/136
TELECOMMUNICATION INFORMATION:
TELEFAX: (213) 955-0440
TELEFAX: (213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17; DB 2; Length 10;
Pred. No. 7e+02;
Trinthes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Stansens, Partick Exic Hugo
APPLICANT: Stansens, Partick Exic Hugo
APPLICANT: Banchers, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laucher, Yves Rene
APPLICANT: Jeapcehe, Yves Rene
APPLICANT: Gensemans, Yannick Georges Jozef
APPLICANT: Gensemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid. US-08-634-641-249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 65.4%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 7e+ Matches 9; Conservative 0; Mismatches
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MEDIUM TYPE: Storage
COMPUTER: STORE STORE OUR COMPUTER: DBM COMPATIBLE OPERATING SYSTEM: IDBM P.C. DOS 5.0 SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/34,641
FILING DATE: APRIL 19, 1996
FILING DATE: OCCODER 17, 1995
APPLICATION NUMBER: 08/46,399
FILING DATE: JUNE 5, 1995
APPLICATION NUMBER: 08/46,397
FILING DATE: JUNE 5, 1995
APPLICATION NUMBER: 08/46,397
FILING DATE: JUNE 5, 1995
APPLICATION NUMBER: 08/46,397
FILING DATE: JUNE 5, 1995
APPLICATION NUMBER: 08/46,380
FILING DATE: JUNE 5, 1995
APPLICATION NUMBER: 08/46,380
FILING DATE: JUNE 5, 1995
APPLICATION NUMBER: 08/46,380
       FILING DATE: OCLOBER 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANDEL:
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 219/136
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-040
TELEPAX: (213) 955-040
INFORMATION FOR SEQ ID NO: 249:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 299, Application US/08634641 Patent No. 5955294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRAGMENT TYPE: internal fragment FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CXXXXXXX 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXXXXXXXX 9
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US-08-634-641-299
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Gaps
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GENERAL INFORMATION:
APPLICANT: Visual, George Phillip
APPLICANT: Visual, Jetnick Enic Hugo
APPLICANT: Genseen, Joris Hilda Lieven
APPLICANT: Laroker's Marc Josef
APPLICANT: Laroker's Marc Josef
APPLICANT: Laroker's Yeak Rose
APPLICANT: Genseens. Yannick Georges Jozef
APPLICANT: Genseens. Yannick Georges Jozef
APPLICANT: Genseens. Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Genseens: Josef
CORRESPONDENCE ADDRESS:
APPLICANT: Genseens: Josef
CORRESPONDENCE ADDRESS:
APPLICANT: Genseens: Josef
CORRESPER: Genseens: Josef
CONGUTER: Jo
                                                                              Length 10;
                                                                                                                                                        0; Indels
                                                                     65.4%; Score 17; DB 2;
100.0%; Pred. No. 7e+02;
:ive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 200, Application US/09249471
Patent No. 6040441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 200: SEQUENCE CHARACTERISTICS: LENGTH: 10 amino acids
TYPE: amino acid
                                                                              Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                              1 CXXXXXXXX 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 23
US-09-249-471-200
        US-08-286-861-42
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US-082-886-81-42
Sequence 81.42
Patent No. 5981478
Fatent No. 5981478
Fatent No. 5981478
Fatent No. 5981478
Fatent No. 5981478

APPLICANT: Rucelahtt, Erkki
APPLICANT: Rolenahtt, Erkki
APPLICANT: Racelahtt, Erkki
APPLICANT: Garbell Erkki
TITLE OF INVENTION: No. 5981478el Integrin-Binding Peptides
NUMBER OF SEGURNES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEB: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STREET: Galifornia
COUNTRY: USA
ZIP: 92122
COMPUTER READBALE FORM:
MEDIUM TYPE: Florey disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,861
FILING DATE: 04-AUG-1994
FLING DATE: 04-NOV-1993
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: US 08/158,001
FILING DATE: 10-AUNCHINEMATION:
TELEPRONE/LOCKET NUMBER: 131,815
REFERENCE/COKET NUMBER: 131,815
REFERENCE CHARACTERISTICS:
LINFORMATION FOR SEQ 110 NO: 42:
ENDUCHE. 10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AUTO-10-AU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: Xaa in locations 2 to 10 is an CTHER INFORMATION: amino acid. US-08-634-641-352
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTONBY/ABENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTAATION NUMBER: 219/136
TELECHOMUNICATION INFORMATION:
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CXXXXXXXX 9
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Gaps
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APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jenscher, Jeurent Stephane
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, NewArode-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: NHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                    65.4%; Score 17; DB 3; Length 10; 100.0%; Pred. No. 7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                           CTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid. US-09-249-471-249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vlasuk, George Phillip
Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: atorage
COMPUTER: 18M Compatible
OPERATING SYSTEM: 1BM P.C. DoS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,471
FILING DATE:
APPLICATION NUMBER: US/09/249,471
FILING DATE: APTI 17, 1997
APPLICATION NUMBER: PCT/US95,13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/466,399
FILING DATE: JUNE 5, 1995
APPLICATION NUMBER: 08/466,397
FILING DATE: JUNE 5, 1995
APPLICATION NUMBER: 08/466,397
FILING DATE: JUNE 5, 1995
APPLICATION NUMBER: 08/461,965
ATTORAGE AND NUMBER: 08/461,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 299, Application US/09249471
Parent No. 6040441
GENERAL INFORMATION:
                                                                                              TYPE: amino acid
TOPOLOGY: linear
FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ifth Street
                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    633 West Fi
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CXXXXXXX 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CXXXXXXXX
         67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
STREET:
      TELEX:
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APPLICANT: Stansens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Laucereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jesperst, Laurent Stephane
APPLICANT: Jesperst, Laurent Stephane
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter M.
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                        65.4%; Score 17; DB 3; Length 10; 100.0%; Pred. No. 7e+02; Live 0; Mismatches 0; Indels
                                                                                           ) OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid. US-09-249-471-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PELLORATION DATA:
PRICATION NUMBER: 08/809,455
PILING DATE: APPLID: 1,1995
APPLICATION NUMBER: PCT/U895/13231
APPLICATION NUMBER: PCT/U895/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: June 5, 1995
APPLICATION NUMBER: 1994
ATTORNEY/AGENT INFORMATION:
RAPLICATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-249-471-249
; Sequence 249, Application US/09249471
; Patent No. 6040441
TOPOLOGY: linear
FRAGMENT TYPE: internal fragment
FEATURE:
                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: Lyon & 633 West F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                    1 CXXXXXXX 9
                                                                                                                                                                                                                                                                                                                                                                                                            1 CXXXXXXX 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                              Query Match
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0
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APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Stanssens, Joris Hilda Lieven
APPLICANT: Lavenerey, Marc Josef
APPLICANT: Lavenerey, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Laroche, Yves Rene
APPLICANT: Ganemans, Yannick Georges Jozef
APPLICANT: Ganemans, Yannick Georges Jozef
APPLICANT: Bergum, Peter W
APPLICANT: Bergum, NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: Lyon
K Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUMTRY: U.S.
ZIP: 90771
COMMUTER READABLE FORM:
MEDIUM TYPE: Storage
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.4%; Score 17; DB 3; Length 10; 100.0%; Pred. No. 7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Xaa in locations 2 to 10 is CHER INFORMATION: amino acid. US-09-249-471-352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,472
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/609,455
FILING DATE: APTI 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: OCCODER 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: OCCODET 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 489-1600
TELEFACE (213) 955-0440
INFORMATION FOR SEQ ID NO: 352:
LENGTH: 10 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 200, Application US/09249472 Patent No. 6046318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXXXXXXXX 9
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US-09-249-472-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 352, Application US/09249471
; Sequence 352, Application US/09249471
; Patent No. 6040441
; Patent No. 6040441
; APPLICANT: Vlasuk, George Phillip
APPLICANT: Lauvereys, Marc Josef
APPLICANT: Lauvereys, Marc Josef
APPLICANT: Laropers, Laurent Stephane
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Moyle, Matchew
APPLICANT: Moyle, Matchew
APPLICANT: Moyle, Matchew
APPLICANT: Bergum, Peter W
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: OF TITLE OF TOWNERSPONDENCE ADDRESSS:
ADDRESSOURCESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 65.4%; Score 17; DB 3; Length 10; Best Local Similarity 100.0%; Pred. No. 7e+02; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid. US-09-249-471-299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,471
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APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: OCCODER 17, 1995
FILING DATE: June 8, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
APPLICATION NUMBER: 08/486,397
         30,158
3R: 216/270
                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
FRAGMENT TYPE: internal fragment
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216//
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: (7-310
INFORMATION FOR SEQ ID NO: 299:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: June 5
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CXXXXXXXX 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CXXXXXXX 9
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Gaps

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FILING DATE: Under 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: Occober 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE I.
REPERENCE/DOCKET NUMBER: 216/270
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
INFORMATION FOR SEQ ID NO: 200:
SEQUENCE CHARACTERICIS:
LENGTH: 10 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY; linear FRAGMENT TYPE: internal fragment
```

ö 65.4%; Score 17; DB 3; Length 10; 100.0%; Pred. No. 7e+02; Live 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 9; Conservative

OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid. US-09-249-472-200

1 CXXXXXXX 9

RESULT 28
US-09-249-472-249
Sequence 249, Application US/09249472
Sequence 249, Application US/09249472
Fatent No. 6046318
GENERAL INFORMATION:
APPLICANT: Stansens, Patrick Eric Hugo
APPLICANT: Messens, Oris Hilda Lieven
APPLICANT: Laroche, Yves Rene
APPLICANT: Laroche, Yves Rene
APPLICANT: Laroche, Yves Rene
APPLICANT: Laroche, Ves Rene
APPLICANT: Bargum, Pannick Georges Jozef
APPLICANT: Bergum, Peter W
APPLICANT: Bergum, Peter W
APPLICANT: Bergum, NamATONE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE: ADDRESS:

ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700 CITY: Los Angeles STATE: California U.S.A. COUNTRY:

CONTENT DOTAL

CONTENT READALE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.0" OPPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PERECE 5.1
CURRENT APPLICATION NUMBER: US/09/249,472
FILING DATE:

PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/809,455

OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid. US-09-249-472-249 FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: OCTOBER 17, 1995
APPLICATION NUMBER: 08/46,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,307
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,196
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,196
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/26,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE.
REPRENCEY/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 469-1600
TELEPACE: 67-3510
INFORMATION FOR SEQ ID NO: 249:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acids
TYPE: ALLOGATION INFORMATION:
TELESTICH 10 amino acids
TYPE: amino acids TOPOLOGY: linear FRAGMENT TYPE: internal fragment FEATURE:

Ouery Match

Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 9; Conservative 0; Mismatches 0; Indels

.. 0

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1 CXXXXXXXX 9

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US-U9-249-444-42-29
US-U9-249-444-42-29
US-U9-249-444-42-29
US-US-249-44-42-29
US-US-249-44-42-29
US-US-24-42-29
US-US-24-42-29
US-US-24-42-29
US-24-42-29
US-24-4 RESULT 29 US-09-249-472-299

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1

```
Sequence 39, Application US/08862855

Sequence 39, Application US/08862855

Sequence 39, Application US/08862855

GENERAL INFORMATION:
APPLICANT: Rucelahti, Erkki
APPLICANT: Pasqualini, Renata
ITILE OF INVENTION: Method of Identifying Molecules That
ITILE OF INVENTION: Home to a Selected Organ in Vivo
NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:
ADDRESSE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COMPUTRY: United States

ZIP: 92122
COMPUTRY: INH GC Compatible
COMPUTRY: ISM PC Compatible
COMPUTRY: SAN PROBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTRY: ISM PC Compatible
COMPUTRY: SAN PROBABLE FORM:
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 65.4%; Score 17; DB 3; Length 10; Best Local Similarity 100.0%; Pred. No. 7e+02; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid.

US-09-249-472-352
                                                                                                                                                                                                            PRICA APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: APRIL 17, 1997
APPLICATION NUMBER: PCT/USSS/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/48,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,390
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,300
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,965
FILING DATE: October 18, 1994
ATTORNEY, AGENT INFORMATION:
RECISTRATION NUMBER: 30,158
REPERRENCE/DOCKET NUMBER: 216/270
TELLEPAK: (213) 955-0440
            COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,472
FILLIG DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 10 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Decouple 17-35.

Sequence 352. Application US/09249472

Patent No. 6046318

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Vlasuk, George Phillip

APPLICANT: Stanssens, Patrick Eric Hugo

APPLICANT: Lauwereys, Marc Josef

APPLICANT: Laroche, Yves Rene

APPLICANT: Laroche, Yves Rene

APPLICANT: Laroche, Yves Rene

APPLICANT: Bespens, Tannick Georges Jozef

APPLICANT: Bespens, Pater W

APPLICANT: Bespens, Peter W

APPLICANT: Bespens, Peter W

APPLICANT: Bespens, Peter W

APPLICANT: PROTEIN

TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT

TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 Weet Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Xaa in locations 2 to 10 is ; OTHER INFORMATION: amino acid. US-09-249-472-299
                                                          FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/809,455

FILING DATE: April 17, 1997

APPLICATION NUMBER: PCT/US95/13231

FILING DATE: October 17, 1995

APPLICATION NUMBER: 08/486,399

FILING DATE: Unne 5, 1995

APPLICATION NUMBER: 08/466,397

FILING DATE: Unne 5, 1995

APPLICATION NUMBER: 08/461,965

FILING DATE: Unne 5, 1995

APPLICATION NUMBER: 08/461,965

FILING DATE: Unne 5, 1995

APPLICATION NUMBER: 08/461,965

FILING DATE: October 18, 1994

ATTORNEY AGENT INPORMATION:

NAME: BIGGS, SUZANNE L.

REGISTRATION NUMBER: 30,158

REFERENCE/DOCKET NUMBER: 30,158

TELECHONE: (213) 489-1600

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 299:
SEQUENCE CHARACTER: STICS:
LENGTH: 10 amino acids
                        APPLICATION NUMBER: US/09/249,472 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE: internal fragment
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CXXXXXXX 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXXXXXXXX 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 30
US-09-249-472-352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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CATERT NO. 6087487

GENERAL INFORMATION:

APPLICANT: Vlauk, George Phillip
APPLICANT: Stansens, Patrick Eric Hugo
APPLICANT: Lauwerey, Marc Josef
APPLICANT: Lauwerey, Marc Josef
APPLICANT: Lauwerey, Warc Josef
APPLICANT: Lauwerey, Warc Josef
APPLICANT: Lauwerey, Wanchew
APPLICANT: Gensemans, Vannick Georges Jozef
APPLICANT: Bergim, Peter W,
APPLICANT: Bergim, Peter W,
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: Solic & Lyon
STREET: Solic & Angeles
STREET: California
COUNTRY: California
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
65.4%; Score 17; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Xaa in locations 2 to 10 is OTHER INFORMATION: amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMFUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WOR'D PATA:
PILING DATE: OCCULLED APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/45,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/45,100
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/45,110
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/25,110
FILING DATE: JUNE 5, 1995
APPLICATION NUMBER: 08/25,110
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REPERBONCE/DOCKET NUMBER: 216/270
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELEPHONE: (213) 955-0440
TELEPHONE: GASTONE NO. 200: SEQUENCE GRARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/249,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 33
US-09-249-451-249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-249-451-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Visuk, George Phillip
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Laroche, Yes Rene
APPLICANT: Laroche, Yes Rene
APPLICANT: Janoche, Yes Rene
APPLICANT: Janoche, Yes Rene
APPLICANT: Janoche, Yes Rene
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
APPLICANT: Bergun, Peter N
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 631 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 65.4%; Score 17; DB 3; Length 10; Best Local Similarity 100.0%; Pred. No. 7e+02; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: SUITE 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READBLE FORM:
MEDIUM TYPE: 3: Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                      FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,710
FILING DATE: 11-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/813,273
FILING DATE: 10-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: CAMDDell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2621
TELEPHONE: (619) 535-8949
INFORMATION (619) 535-8949
INFORMATION CATACHERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/13231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/249,451
        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/862,855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 200, Application US/09249451
Patent No. 6087487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: peptide US-08-862-855-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CXXXXXXXX 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-249-451-200
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us-10-046-922-33.closed.rai

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COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFFWARE: Word Perfect 5.1
CURRENT APPLICATION NATA:
PILING DATE:
PRION APPLICATION NATA:
APPLICATION NUMBER: US/09/249,451
FILING DATE: APPLICATION NUMBER: 08/809,455
APPLICATION NUMBER: 08/80,397
APPLICATION NUMBER: PCT/US95/13231
APPLICATION NUMBER: PCT/US95/13231
APPLICATION NUMBER: 08/486,397
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/466,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/466,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: June 5, 1995
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 216/270
TELEFAX: 67-3510
INFORMATION POR SEQ ID NO: 299:
TELEFAX: 67-3510
INFORMATION: AMA INFORMATION:
FRAGMENT TYPE: INTERTAL FRAGMENT
FRAGMENT TYPE: INTERTAL INTERTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXXXXXXXX 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-249-451-299
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APPLICANT: Stansens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilde Lieven
APPLICANT: Messens, Joris Hilde Lieven
APPLICANT: Laroche, Yves Rene
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Moyle, Matthew
APPLICANT: Bergun. Peter N.
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
ITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 65.4%; Score 17; DB 3; Length 10; Best Local Similarity 100.0%; Pred. No. 7e+02; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid.
                           PRIOR DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/809,455
FILING DATE: APPLICATION NUMBER: 07/1095/13231
APPLICATION NUMBER: PCT/US95/13231
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: June 5, 1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELEFAX: (213) 989-1600
TELEFAX: (213) 989-1600
TELEFAX: (213) 989-1600
TELEFAX: (213) 985-0440
INFORMATION FOR SEQ ID NO: 249:
SEQUENCE CHARACTER/STICS:
LENGTH: 10 amino acids
TYPER: manno acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 299, Application US/09249451
Patent No. 6087487
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CXXXXXXXX 9
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Sequence 352, Application US/09249451
; Sequence 352, Application US/09249451
; Patent No. 6087487
; GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
APPLICANT: Lauwarreys, Marc Josef
APPLICANT: Lauwarreys, Marc Josef
APPLICANT: Lauwarreys, Marc Josef
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Matthew
APPLICANT: Matthew
APPLICANT: Bergum, Peter W.
ITILE OF INVENTION: INHIBITORS AND ANTICOAGULANT
ITILE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORDESSEDANTENCES: 356
                                                                                                                                 Query Match 65.4%; Score 17; DB 3; Length 10; Best Local Similarity 100.0%; Pred. No. 7e+02; Matches 9; Conservative 0; Mismatches 0; Indels
OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid.
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Gaps
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TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Moyle, Matthew
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
ZIP: 90071
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 15." Diskette, 1.44 Mb
MEDIUM TON THE 17, 1997
MEDIUM DATE: Unne 5, 1995
APPLICATION NUMBER: 08/46, 397
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/46, 965
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/46, 965
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/46, 965
APPLICATION NUMBER: 08/46, 965
APPLICATION NUMBER: 08/40, 965
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/40, 965
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/40, 965
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/40, 965
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/20, 10
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/20, 10
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/20, 10
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/20, 10
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/20, 10
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/20, 10
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/20, 10
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/20, 10
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/20, 10
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/20, 10
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/20, 10
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/20, 10
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/20, 10
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/20, 10
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/20, 10
FILING DATE: Unne 5, 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 10 amino acids
amino acid
3Y: linear
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-809-455-200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vlasuk, George Phillip
Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yamnick Georges Jozef
Moyle, Matthew
                                                       ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 8 torage
COMPUTER: IBM COMPACTIBLE
COMPUTER: NOT PERFECT 5.1
CUMBENT APPLICATION DATA:
RILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                           PRILING DATE:

APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: OCCODER 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: JUNE 5, 1994
ATTONNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERRENCE/DOCKET NUMBER: 216/270
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 352:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 200, Application US/08809455; Patent No. 6090916
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip APPLICANT: Stanssens, Patrick Eric H APPLICANT: Lauwereys, Marc Josef APPLICANT: Lauwereys, Marc Josef APPLICANT: Laroche, Yves Rene APPLICANT: Jespers, Laurent Stephane; APPLICANT: Gensemans, Yannick George APPLICANT: Movle, Matthew APPLICANT: Bergum, Peter W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 3
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US-08-809-455-200
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APPLICANT: Bergum, Peter W.

TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSE: 1, you & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 65.4%; Score 17; DB 3; Length 10; Best Local Similarity 100.0%; Pred. No. 7e+02; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTYER: 0.5.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: 1.5" DISKETS

COMPUTER: IBM Compatible

OSPERATING SYSTEM: 18M P.C. DOS 5.0

SOFTWARE: Word berfect 5.1

APPLICATION NUMBER: 901/95/13231

PHLING DATE: ADDIEST: 1995

APPLICATION NUMBER: 08/46,399

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/46,397

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/46,397

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/46,380

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/326,110

FILING SATE NUMBER: 30,158

REFERENCE/DOCKET NUMBER: 30,158

REFERENCE/DOCKET NUMBER: 30,158

REFERENCE/ORNINICATION INFORMATION:

TELERHAX: (213) 955-0440

INFORMATION FOR SEQ ID NO: 299:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 352, Application US/08809455
Patent No. 6090916
GENERAL INFORMATION:
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Patrick Eric Hugo
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Warc Josef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE: internal fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXXXXXXXX 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . Vlasuk, George Phillip
. Stanssens, Patrick Eric Hugo
. Messens, Joris Hilda Lieven
. Lauwereys, Marc Josef
. Laroche, Yves Rene
. Jespers, Laurent Stephane
. Gansemans, Yannick Georges Jozef
. Moyle, Matthew
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION NUMBER: US/08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/466,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/301
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/301
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/301
FILING DATE: June 5, 1995
APPLICATION NUMBER: 30,188
REFERENCE/DOCKET NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOSEPH CONTROL OF SECUROR SECU
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TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                      STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
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0; Gaps

us-10-046-922-33.closed.rai

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APPLICANT: Lauvereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jaroche, Yves Rene
APPLICANT: Jaroche, Yves Rene
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 65.4%; Score 17; DB 3; Length 10; Best Local Similarity 100.0%; Pred. No. 7e+02; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: XAA in locations 2 to 10 is an OTHER INFORMATION: amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Storage COMPUTER: Storage COMPUTER: IEBM COMPATIBLE COMPUTER: IEBM COMPATIBLE COMPUTER: SOSTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/249,461
FILING DATE: WORD COLOGER: US/09/455
APPLICATION NUMBER: 08/809,455
APPLICATION NUMBER: 08/86,399
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/466,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/466,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: June 5, 1995
APPLICATION NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 67-3510
INFORMATION FOR SEG ID NO. 200:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acids
                                                     Messens, Joris Hilda Lieven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXXXXXXXX 9
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US-09-249-461-249
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APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum. Peter M.
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 Weet #1701
CITY. TO MILE #4700
CITY. TO MILE #4700
CITY. TO MILE #4700
CITY. TO MILE #4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.4%; Score 17; DB 3; Length 10; 100.0%; Pred. No. 7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid. US-08-809-455-352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM;
MEDIUM TYPE: ST.S." Diskette, 1.44 MD
MEDIUM TYPE: STORAGE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD BATE:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/809,455
FILING DATE: October 17, 1997
APPLICATION NUMBER: OG/46,399
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/46,399
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/46,397
APPLICATION NUMBER: 08/46,397
APPLICATION NUMBER: 08/46,399
APPLICATION NU
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Patent No. 6096877
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanssens, Patrick Eric Hugo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CXXXXXXXX 9
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US-09-249-461-200
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1 CXXXXXXX 9

Sequence 249, Application US/09249461

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APPLICANT: Vlassens, Patrick Eric Hugo
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lawwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Laroche, Yves Rene
APPLICANT: Ganesmans, Yannick Georges Jozef
APPLICANT: Ganesmans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter M
APPLICANT: Bergum, Peter M
APPLICANT: Pergum, Peter M
APPLICANT: PROTEND: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Xaa in locations 2 to 10 is OTHER INFORMATION: amino acid.
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ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IEM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,461
FILING DATE: April 17, 1995
APPLICATION NUMBER: PCT/US95/1321
APPLICATION NUMBER: PCT/US95/13231
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OCCUPE: SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
APPLICANT: Vlasuk, George Phillip
APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Georges, Laurent Stephane
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Seluter Moyle, Lyon
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE
TITLE OF INVENTION: NEMATODE-EXTRACTED
TITLE OF INVENTION: NEMATODE-EXTRACTED
CORRESPONDENCE ADDRESSES:
ADDRESSES: Loon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STREET: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.4%; Score 17; DB 3; Length 10; 100.0%; Pred. No. 7e+02; 1.ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTER READBLE FORM:

COMPUTER READBLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: STORAGE
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,461
FILING DATE: October 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,390
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/36,110
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/36,110
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/36,110
FILING DATE: June 5, 1995
APPLICATION NUMBER: 30,188
REFERENCE/DOCKET NUMBER: 30,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-249-461-249
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Length 10;

65.4%; Score 17; DB 3;

US-09-249-461-299 Query Match

Gaps . 0

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Gaps
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APPLICANT: Assens, Joris Hilda Lieven
APPLICANT: Lawereys, Marc Josef
APPLICANT: Lawereys, Marc Josef
APPLICANT: Lawereys, Marc Josef
APPLICANT: Ganeemans, Yannick Georges Jozef
APPLICANT: Ganeemans, Yannick Georges Jozef
APPLICANT: MOYLE, Matthew
APPLICANT: MOYLE, Matthew
APPLICANT: Bergum, Peter M
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                            Query Match

Best Local Similarity 100.0%; Pred. No. 7e+02;

Matches 9; Conservative 0; Mismatches 0; Indels
) OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid. US-09-249-461-352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 8corage
COMPUTER: 1EM Compatible
OPERATING SYSTEM: 1EM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRILING DATE:
PRILING DATE:
PRILING DATE:
PRILING DATE:
PRILING APPLICATION NUMBER:
PULING DATE: APATI 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/46,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,390
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,300
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: October 18, 1994
ATTORNEY/AGENT INPORMATION:
REGISTATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 200:
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 200, Application US/09249448 Patent No. 6121435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vlasuk, George Phillip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIRET: Suite
SITY: Los Angeles
SIATE: California
                                                                                                                                                                                                                     1 CXXXXXXXX 9
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                                             Gaps
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                                                                                                                                                                                                                                                                                                                      APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Stanssens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Laroche, Yves Rene
APPLICANT: Jaroche, Yves Rene
APPLICANT: Gansemans, Yamnick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, Matthew
APPLICANT: Moyle, NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Layon & Lyon
STREET: 633 West Fifth Street
STREET: 633 West Fifth Street
                                             Indels
                  Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRILICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: APril 17,1997
APPLICATION NUMBER: PCT/U895/13231
APPLICATION NUMBER: PCT/U895/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: JUNE 5, 1995
APPLICATION NUMBER: 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZAMID L.
REGISTRATION NUMBER: 216/270
TELECOMMINICATION NUMBER: 216/270
TELECOMMINICATION NUMBER: 216/270
TELECOMMINICATION NUMBER: 216/270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 90071
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,461
FILING DATE:
                                                                                                                                                                                                                                                                Sequence 352, Application US/09249461 Patent No. 6096877 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    internal fragment
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TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 352:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amin Type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Los Angeles
California
                                                                                              1 CXXXXXXXX 9
                                                                                                                                            1 CXXXXXXXX 9
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FRAGMENT TYPE:
FEATURE:
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                                                                                                                                                                                                                                                   -09-249-461-352
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Gaps
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GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanssens, Datrick Eric Hugo
APPLICANT: Messens, John Hilda Lieven
APPLICANT: Lauvereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Scephane
APPLICANT: Gensemans, Yannick Georges Jozef
APPLICANT: Gensemans, Yannick Georges Jozef
APPLICANT: Bergum, Peter W,
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                       65.4%; Score 17; DB 3; Length 10; 100.0%; Pred. No. 7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 10;
                                                                                                                                                                                                                                                                                                        Xaa in locations 2 to 10 is an amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: Salie 4700
CITY: Los Angeles
CITY: Los Angeles
COUNTRY: U.S.A.
ZIP: 9001
COMPUTER READABLE FORM:
WEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: STORAGE
COMPUTER: IBM Compatible
COMPUTER: APPLICATION NUMBER: 08/486,399
FILING DATE: Oute 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
APPLICATION NUMBER: 08/461,965
APPLICATION NUMBER: 08/461,965
APPLICATION NUMBER: 08/461,965
APPLICATION NUMBER: 08/361,100
FILING DATE: Oute 6, 1995
APPLICATION NUMBER: 08/361,100
FILING DATE: OCCODER 18, 1995
APPLICATION NUMBER: 08/361,100
FILING DATE: OUTE 6, 1995
APPLICATION NUMBER: 08/361,100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 299, Application US/09249448
Patent No. 6121435
                                                                                                                                                                                                          TOPOLOGY: linear
FRAGMENT TYPE: internal fragment
FEATURE:
                          TELEFAX: (213) 955-0440
TELEX: 67-3510
INPORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
(213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
COTHER INFORMATION:
US-09-249-448-249
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   TELEPHONE:
TELEFAX: (
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; Sequence 249, Application US/09249448
; Pattent No. 6121435
; GENERAL INFORMATION:
    APPLICANT: Vlasuk, George Phillip
    APPLICANT: Stansens, Patrick Eic Hugo
    APPLICANT: Lauwereys, Marc Josef
    APPLICANT: Lauwereys, Marc Josef
    APPLICANT: Jaroche, Yves Rene
    APPLICANT: Jaroche, Vres Rene
    APPLICANT: Jaroche, Matthew
    APPLICANT: Moyle, Matthew
    TITLE OF INVENTION: NEWATODE-EXTRACTED SERINE PROTEASE
    TITLE OF INVENTION: NEWATODE-EXTRACTED SERINE
    TITLE OF INVENTION: NEWATODE-EXTRACTED SERINE
    TITLE OF INVENTION: PROTEIN
    NUMBER OF SEQUENCES: 356
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                               FEATURE:
OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid.
US-09-249-448-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRILICATION DATA:
APPLICATION NUMBER:
PRICATION NUMBER:
PRICATION NUMBER:
PCT 1995
APPLICATION NUMBER:
PCT 1995
APPLICATION NUMBER:
PCT 1995
APPLICATION NUMBER:
PCT 1995
APPLICATION NUMBER:
PTILING DATE:
PTILING DATE:
APPLICATION NUMBER:
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PTILING DATE:
PTILING DATE:
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APPLICATION NUMBER:
PTILING DATE:
APPLICATION NUMBER:
PTILING DATE:
ATTORNEY/AGENT INPORMATION:
TELECOMMUNICATION NUMBER:
PTILING DATE:
PTILING DATE:
ATTORNEY/AGENT INPORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                 internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
         LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                              1 CXXXXXXX 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CXXXXXXXX
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RESULT

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Sequence 39, Application US/09226985

Sequence 39, Application US/09226985

Sequence 39, Application US/09226985

Sequence 39, Application US/09226985

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid.
FILING DATE: June 5, 1995
APPLICATION NUMBER: 00/461,965
FILING DATE: June 8, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENI INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 20,158
REPERBNCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAME (213) 489-1600
TELECAME (713) 955-0440
TELEX: 67-3210
INFORMATION FOR SEQ ID NO: 352:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acid
TOPOLOGY: linear
FRACHER:
FRACHER: internal fragment
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXXXXXXXX 9
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Sequence 352, Application US/09249448

Patent No. 6121435
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Laroche, Yves Rene
APPLICANT: Daspers, Laurent Stephane
STREET: Suite ATOO
CITY: Los Angeles
STREET: Suite ATOO
CITY: Los Angeles
STREET: Suite ATOO
CUNTRY: U.S.A.
ZIP: 9071
COMPUTER REAABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" DISKETS, 1.000 S.O
SOFTWARE: Word Perfect S.I
CURRENT APPLICATION NUMBER: US/09/249,448
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid. US-09-249-448-299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICALL...
PRIJUG DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
              ATTORNEY/AGENT INFORMATION:
NAME: BIGGS. SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/POCKET NUMBER: 216/270
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: (713) 955-0460
INFORMATION FOR SEQ ID NO: 299: SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CXXXXXXX 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CXXXXXXXX 9
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US-09-249-448-352
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CHENERAL INFORMATION:
APPLICANT: Stanseens, Patrick Eric Hugo
APPLICANT: Stanseens, Patrick Eric Hugo
APPLICANT: Stanseens, Jorie Hilde Lieven
APPLICANT: Messens, Jories Hilde Lieven
APPLICANT: Laroche, Yves Rene
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gespers, Laurent Stephane
APPLICANT: Bergum, Peter N.
APPLICANT: Bergum, Peter N.
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon
STREET: Suite 4700
CTREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid. US-09-249-473-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTERN TO U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: 1.5" DISKETS
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBMP.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: ADMER: 08/80,399
FILING DATE: Olune 5, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,965
APPLICATION NUMBER: 08/46,996
APPLICATION NUMBER: 08/46,999
APPLICATION NUMBER: 08/46,999
APPLICATION NUMBER: 08/46,999
APPLICATION
                                                                                                                                                                                           Sequence 200, Application US/09249473
Patent No. 6534629
GENBRAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                                                                                                                                   US-09-249-473-200
                                                                                                                                   RESULT 50
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 39, Application US/09227906
Patent No. 6306365
GENERAL INFORMATION:
APPLICANT: Rucelahti, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Method of Identifying Molecules That
TITLE OF INVENTION: Method of Selected Organ In Vivo
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                           Ouery Match 65.4%; Score 17; DB 3; Length 10; Best Local Similarity 100.0%; Pred. No. 7e+02; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 65.4%; Score 17; DB 4; Length 10; Best Local Similarity 100.0%; Pred. No. 7e+02; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READSLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPENATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/227,906
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA;

FILING DATE: 11-SEP-1995

FILING DATE: 11-SEP-1995

FILING DATE: 11-SEP-1995

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 08/862,855

FILING DATE: 10-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Campbell. Cathryn A.

REGISTRATION NUMBER: 31,815

TELECOMMUNICATION INFORMATION:

TELECHHONE: (619) 535-8949

INFORMATION FOR SEO ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDAR.:
STREET: 43/0 _.
CITY: San Diego
SIATE: California
_____RY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-227-906-39
                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-226-985-39
                                                                                                                                                                                                                                                                                                                                                                                                                              1 CXXXXXXX 9
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1 CXXXXXXX 9

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                          AFBLICANT: Vlasuk, George Phillip
AFBLICANT: Stanssens, Patrick Eric Hugo
AFBLICANT: Lauwereys, Marc Josef
AFBLICANT: Lauwereys, Marc Josef
AFBLICANT: Laurent Stephane
AFBLICANT: Laurent Stephane
AFBLICANT: Gansenans, Yannick Georges Jozef
AFBLICANT: Moyle, Matthew
AFBLICANT: Moyle, Matthew
AFBLICANT: Moyle, Matthew
AFBLICANT: Bergum, NEMATOBE-EXTRACTED SERINE FROTEASE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF SQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon F TERM
                                                                                                                           65.4%; Score 17; DB 4; Length 10;
100.0%; Pred. No. 7e+02;
tive 0; Mismatches 0; Indels
  ; FEATURE:
; OTHER INFORMATION: Xaa in locations 2 to 10 is an
; OTHER INFORMATION: amino acid.
US-09-249-473-249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER REABBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
CORPTING SYSTEM: IBM P.C. DOS 5.0
SOFTMARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRILING DATE:
PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/09/455
FILING DATE: APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,965
APPLICATION NUMBER: 08/46,965
APPLICATION NUMBER: 08/46,965
APPLICATION NUMBER: 08/46,965
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 299:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (213) 955-0440
                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 9; Conservative
                                                                                                                                                                                                                               1 CXXXXXXXX 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 California
: U.S.A.
                                                                                                                                                                                                                                                                               1 CXXXXXXX 9
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CITY: LOS P
STATE: Cali
COUNTRY: U.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                             US-09-249-473-299
                                                                                                                                                                                                                                                                                                                                                          RESULT 52
                                                           Gaps
Query Match
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BIJON, PEECH W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: Suite 4700
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                             Vlasuk, George Phillip
Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Gespers, Laurent Stephane
Gansemans, Yamnick Georges Jozef
Moyle, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: ISM Compatible
COPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WOOM PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRICIATION NUMBER: 08/609,455
FILING DATE: April 17, 1995
APPLICATION NUMBER: PCT/U855/13231
APPLICATION NUMBER: PCT/U855/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/466,397
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/36,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30 158
REFERENCE/DOCKET NUMBER: 30 158
REFERENCE/DOCKET NUMBER: 30 158
TELEPRAS: (213) 489-1600
TELEPRAS: (213) 955-0440
                                                                                                                                                                                                                                                                       Sequence 249, Application US/09249473
Patent No. 6534629
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanssens, Patrick Eri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 249:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
                                                                                                   1 CXXXXXXX 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Los Angeles
STATE: California
                                                                                                                                                 1 CXXXXXXXX 9
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                                                                                                                                                                                                                         RESULT 51
US-09-249-473-249
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CITY: L
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GENERAL INFORMATION:

GENERAL INFORMATION:
APPLICANT: Googe P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Marc J. Lauvereys,
APPLICANT: Yes R. Laroche, Lauvent S. Jespers,
APPLICANT: Yes R. Laroche, Lauvent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORESPONDENCE ADDRESS: 356
CORRESPONDENCE ADDRESS: 356
CITY: Los Angeles
STREET: Salte 4700
CITY: Los Angeles
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: June 5.1995
COMPUTER: June 5, 1995
COMPUTER: June 5, 1995
CLASSIFTCATION NUMBER: 08/326,110
FILING DATE: June 5, 1995
CLASSIFTCATION NUMBER: 08/326,110
FILING DATE: June 5, 1995
CLASSIFTCATION NUMBER: 213/268
FELECOMMUNICATION INFORMATION:
NAMN: BIGGS, SUZANNE L.
REGISTATION NUMBER: 213/268
FELECOMMUNICATION INFORMATION:
TELEFAX: 67-3510
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 145:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORMATION: amino acid. US-09-249-473-352
TELECOMMUNICATION INFORMATION:
TELEBRANE: (213) 955-0440
TELERX: 67-3510
INFORMATION FOR SEQ ID NO: 352:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
FRAGMENT TYPE: internal fragment
FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-465-380-145
; Sequence 145, Application US/08465380
; Patent No. 5863894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: internal fragment FEATURE:
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LENGTH: 10 amino acids
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CEMERAL INFORMATION:
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Gesens, Joris Hilds Lieven
APPLICANT: Laveereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Laroche, Yves Rene
APPLICANT: Genemans, Yannick Georges Jozef
APPLICANT: Genemans, Yannick Georges Jozef
APPLICANT: Bergum, Peter W
APPLICANT: Bergum, Peter W
APPLICANT: Bergum, Nematobe-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: APONE
TITLE OF INVENTION: APONE
ATTER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 Meet Fifth Street
                                                                                                                                                                                                                                                                                                                          Query Match

65.4%; Score 17; DB 4; Length 10;

Best Local Similarity 100.0%; Pred. No. 7e+02;

Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                         CTHER INFORMATION: Xaa in locations 2 to 10 is an OTHER INFORWATION: amino acid. US-09-249-473-299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRETAINS SYSTEM: IBM P.C. DOS S.O SORRETAING SYSTEM: IBM P.C. DOS S.O SORRETAING SYSTEM: IBM P.C. DOS S.O SORRETAIN BETFECT 5.1
CURRETA APPLICATION DATA:
PRILING DATE: WOLD BATA:
APPLICATION NUMBER: US/09/455.
FILING DATE: APTI 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: OCCODET 17, 1995
APPLICATION NUMBER: 08/466,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/466,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/466,396
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/466,365
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: OCCODET 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANDE L.
RESESTRATION NUMBER: 30,158
RESESTRATION NUMBER: 216/270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 352, Application US/09249473
Patent No. 6534629
                                            SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
FRAGMENT TYPE: internal fragment
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXXXXXXX 9
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4 CXXXXXX 10

Xaa in locations 1 to 3 and 5 to 10 is an amino acid.

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Length 10;
                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: GOOTGE P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yees R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESSONDENCES: 356
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Xaa in locations 1 to 3 and OTHER INFORMATION: locations 5 to 10 is an amino OTHER INFORMATION: acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 271, Application US/08465380
Patent No. 5863894
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: George P. Mensens, Marc J. Lauwereys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.7%; Score 15; DB 2; Le
100.0%; Pred. No. 1.9e+03;
:ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" O'BREATE BE
CURRENT APPLICATION DATA:
APPLICATION NUBBER: US/08/465,380
FILING DATE: June 5, 1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: 0ctober 18, 1994
ATTOMEN FORDER: 0.158
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFRENCE/DOCKET NUMBER: 213/268
TELECOMMUNICATION INFORMATION:
TELEFAK: (213) 955-0440
                                                                                                            Sequence 222, Application US/08465380 Patent No. 5863894 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRACMENT TYPE: internal fragment FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 222: SEQUENCE CHARACTERISTICS: LENGTH: 10 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 CXXXXXX 10
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US-08-465-380-271
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                                                                                                                                                                                                                                                                                                                                                                Sequence 173, Application US/08465380
Fatent No. 5863894
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: Joxis H.L. Mensens, Marc J. Lauwereys, APPLICANT: Yes R. Larcche, Laurent S. Jespers, APPLICANT: Yes R. Larcche, Laurent S. Jespers, APPLICANT: Perer W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                              Query Match 57.7%; Score 15; DB 2; Length 10; Best Local Similarity 100.0%; Pred. No. 1.9e+03; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xaa in locations 1 to 3 and locations 5 to 10 is an amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM P.C. DOS 5.0
SOFTWARN: WORD PETCE 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,380
FILING DATE: June 5, 1995
CLASSIFCATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY APPLICATION NUMBER: 213/268
FILING DATE: OCTOBER 18, 1994
ATTORNEY AGENT INFORMATION:
RECISTRATION NUMBER: 213/268
TELECOMMUNICATION INFORMATION:
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: 7-3510
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 10 amino acids
amino acid
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
OTHER INFORMATION:
) OTHER INFORMATION:
) OTHER INFORMATION:
US-08-465-380-145
                                                                                                                                                                                                                                                      CXXXXXX 10
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US-08-465-380-173
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Gaps
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57.7%; Score 15; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Xaa in locations 1 to 3 and OTHER INFORMATION: locations 5 to 10 is an amino OTHER INFORMATION: acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-084-80-478-76
1 Sequence 76, Application US/08480478
2 Sequence 76, Application US/08480478
3 Patent No. 586409
GENERAL INFORMATION P. VLASUK; PATRICK ERIC APPLICANT: HUGO STANSSENS; JORIS HILDA APPLICANT: LIEVEN MESSENS; MACK JOZEF APPLICANT: LAUWERN MESSENS; MACK JOZEF APPLICANT: LAUWERN GEORGES JOZEF APPLICANT: LAUWERN GEORGES JOZEF APPLICANT: YANNICK GEORGES JOZEF APPLICANT: GANSEMANS
TITLE OF INVENTION: COAGULANT PROTEIN NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Lyon & Lyon STREET: 633 Weet Fifth Street STREET: 633 Weet Fifth Street STREET: 633 Weet Fifth Street STREET: Galfornia COUNTRY: Los Angeles STATE: 90071
COMPUTRY: LOS ANGELE FORM: MEDIUM TYPE: 315" Diskette, 1.44 Mb MEDIUM TYPE: SLORAGE
                                                                                 COMPUTER READBLE FORM:

ZIP: 90071

REDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage
COMPUTER: ENORAGE
COMPUTER: IBM COMPALIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PETECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,380
FILING DATE: June 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: OCLOBER 18, 1994
ATTORNEY, AGENT INPORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFREADCENCE/DOCKET NUMBER: 213/268
TELECOMMUNICATION INPORMATION:
TELEPHONE: (213) 955-0440
TELERX: 67-3510
INFORMATION FOR SED ID NO: 325:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TOWNOWN TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE: internal fragment
   Los Angeles
California
XY: U.S.A.
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US-08-480-478-76
   CITY: LOSTATE: CCOUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dp
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Sequence 325, Application US/08465380

Patent No. 5863894

GENERAL INFORMATION:
APPLICANT: General H.L. Mensens, Marc J. Lauwereys, APPLICANT: Yves R. Laroche, Laurent S. Jespers, APPLICANT: Yannick G.J. Gansemans, Matthew Moyle, APPLICANT: Yannick G.J. Gansemans, Matthew Moyle, APPLICANT: Percer W. Bergum:
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 7; Conservative 0; Mismatches 0; Indels
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
CORRESPONDENCE 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
STREET: SLYON & LYON
STREET: SLICE 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: Xaa in locations 1 to 3 and OTHER INFORMATION: locations 5 to 10 is an amino GTHER INFORMATION: acid.
                                                                                                                                                                                                                                                                                            STREET: SLILE 4700
CITY: Los Angeles
STATE: California
CCUMTRY: U.S.A.
ZIP: 90071
COMPUTER READBLE FORM:
MEDIUM TYPE: Storage
COMPUTER: LBM COMPATIBLE
FILING DATE: US/08/465,380

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FRAGMENT TYPE: internal fragment
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E. Lyon & Lyon
633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 10 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 CXXXXXX 10
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US-08-465-380-325
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 173, Application US/08486397;
Patent No. 5866542

GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanseens,
APPLICANT: Joris H.L. Meneens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yanick G.J. Gansemans, Matthew Moyle,
APPLICANT: Yanick G.J. Gansemans, Matthew Moyle,
APPLICANT: Pater W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 357
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: Sai Weet Fith Street
                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Xaa in locations 1 to 3 and 5 corner Information: to 10 is an amino acid. US-08-486-397-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTYER: U.S.T.

ZIP: 90071
ZIP: 90071
ZIP: 90071
ZIP: 90071
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: Storage COMPUTER: 1BM Compatible OPERATING SYSTEM: 1BM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,397
FILING DATE: Unne 5, 1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SULAANEL.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 31,269
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION SEG 10 NO: 173:
SEQUENCE GRARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                 213/269
                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE: internal fragment
FEATURE:
                             REGISTRATION NUMBER: 30,158
REFRENCK/DOCKET NUMBER: 213/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: 67-3310
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 CXXXXXX 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CXXXXXX 7
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US-08-486-397-173
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0
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Patent No. 5866542

GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Larcche, Laurent S. Jespers,
APPLICANT: Pater W. Bergum
ITILE OF INVENTION: NEMATOBE-EXTRACTED ANTICOAGULANT
ITILE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 357

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query March 57.7%; Score 15; DB 2; Length 10; Best Local Similarity 100.0%; Pred. No. 1.9e+03; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Xaa in any location 1 to 3, or OTHER INFORMATION: to 10 is an amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.

ZIP: 90071

ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 8torage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,397
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTONEY AGENT INFORMATION:
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASSES (VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,478
FILING DATE: 06-JUN 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDER: 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANDE: 208/290
FILING DATE: 30,158
REFERENCE/DOCKET NUMBER: 208/290
TELESCHWINICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH 10 amino acids
TYPELES AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIGGS, SUZANNE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 CXXXXXX 10
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US-08-486-397-145
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Sequence 271, Application US/08486397

Patent No. 5866542

GENERAL INFORMATION

APPLICANT: VOIS H.L. Mensens, Marc J. Lauwereys, APPLICANT: VOIS H.L. Mensens, Marc J. Lauwereys, APPLICANT: Yes R. Larconbe, Laurent S. Jespers, APPLICANT: Yes R. Larconbe, Laurent S. Jespers, APPLICANT: Yes R. Larconbe, Laurent S. Jespers, APPLICANT: Peter W. Bergumment Matthew Moyle, APPLICANT: Peter W. Bergumment TITLE OF INVENTION: PROTEIN

TITLE OF INVENTION: PROTEIN

TITLE OF INVENTION: PROTEIN

TITLE OF INVENTION: PROTEIN

TITLE OF INVENTION: S.35

CORRESPONDERSEE: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: 634 West Fifth Street

STREET: 645 West Fifth Street

STREET STREET: 645 West Fifth Street

STREET STREET: 645 West Fifth Street

STREET STREET STREET: 645 West Fifth STREET STREET
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100.0%; Pred. No. 1.9e+03;
ive 0; Mismatches 0; Indel8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 325, Application US/08486397; Patent No. 5866542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100..
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                                                                             4 CXXXXXX 10
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US-08-486-397-325
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                                                                                                                                                                   RESULT 63
US-08-486-397-271
                                                                   QQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 57.7%; Score 15; DB 2; Length 10; Best Local Similarity 100.0%; Pred. No. 1.9e+03; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                               57.7%; Score 15; DB 2; Length 10; 100.0%; Pred. No. 1.9e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Peter W. Bergum
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 357
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTHER INFORMATION: Xaa in locations 1 to 3 and OTHER INFORMATION: locations 5 to 10 is an amino OTHER INFORMATION: acid.
                                                          Xaa in locations 1 to 3 and locations 5 to 10 is an amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
COUNTRY. U.S.A.
ZIP: 90071
COUNTRY. U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 1 Mb
APPLICATION DATE: C. DOS 5.0
PRIOR APPLICATION NUMBER: 08/326,110
APPLICATION NUMBER: 08/326,110
APPLICATION NUMBER: 08/326,110
ATTORNEY AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 213/269
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEPK: 67-3510
INFORMATION FOR SEQ ID NO: 222:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 222, Application US/08486397
Patent No. 5866542
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
FRAGMENT TYPE: internal fragment
FRAGMENT TYPE: internal fragment FEATURE:
                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                       ) OTHER INFORMATION:

) OTHER INFORMATION:

) OTHER INFORMATION:

US-08-486-397-173
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                                                                                                                                                                                                                                                                                                                                                                  4 CXXXXXX 10
                                                                                                                                                                                                                                                                                                                    1 CXXXXXX 7
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Gaps

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Sequence 173, Application US/08486399
; Sequence 173, Application US/08486399
; Patent No. 5866543
; Patent No. 5866543
; Patent No. 5866543
; PAPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: George P. Vancon, Marc J. Lauwereys, APPLICANT: Yees R. Larcche, Laurent S. Jespers, APPLICANT: Yeeler W. Bergum
TITLE OF INVENTION: NEWATODE-EXTRACTED ANTICOAGULANT TITLE OF INVENTION: PROTIEIN
NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
ADDRESSEE: 633 West Fifth Street
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 57.7%; Score 15; DB 2; Length 10; Best Local Similarity 100.0%; Pred. No. 1.9e+03; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Xaa in locations 1 to 3 and 5 OTHER INFORMATION: to 10 is an amino acid. US-08-486-399-145
ADDRESSEE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: Shite 4700
CITY: Los Angeles
CUNTY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
ENDIUM TYPE: Storage
COMPUTER READABLE FORM:
MEDIUM TYPE: Storage
COMPUTER: IBM COMPATIBLE
COMPUTER: MAD TYPE: STORAGE
COMPUTER: MAD TYPE: MAD TYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CXXXXXX 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 145, Application US/08486399; Patent No. 5866543; GENERAL INFORMATION: APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: Goris H.L. Mensens, Marc J. Lauwereys, APPLICANT: Yves R. Larche, Laurent S. Jespers, APPLICANT: Yannick G.J. Gansemans, Matthew Moyle, APPLICANT: Peter W. Bergum; TITLE OF INVENTION: NEWATODE-EXTRACTED ANTICCAGULANT: TITLE OF INVENTION: PROTEIN

TITLE OF INVENTION: PROTEIN

TITLE OF INVENTION: PROTEIN

TITLE OF SECURATES: 356

CORRESPONDENCE ADDRESS:
                                                           APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys, APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys, APPLICANT: Yees R. Laroche, Laurent S. Jespers, APPLICANT: Years R. Laroche, Laurent S. Jespers, APPLICANT: Peter W. Bergum.
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT ILLE OF INVENTION: PROTEIN NUMBER OF SEQUENCES: 357
CORRESPONDENCE ADDRESS:
ADDRESSES: Lyon & Lyon
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ), OTHER INFORMATION: Xaa in locations 1 to 3 and ); OTHER INFORMATION: locations 5 to 10 is an amino ); OTHER INFORMATION: acid.
US-08-486-397-225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READMBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: Disk Competible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PETECT 5.1
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/486,397
FILING DATE: June 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: OCTOBER 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE DOCKET INFORMATION:
TELEFAX: 67.3510
TELEFAX: 67.3510
TELEFAX: 67.3510
TELEFAX: 67.3510
TELEFAX: CANADLE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TENDERAL: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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US-08-486-399-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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Sequence 271, Application US/08486399;
Patent No. 5866543;
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Yors R. Laroche, Laurent S. Jespers,
APPLICANT: Yaves R. Laroche, Laurent S. Jespers,
APPLICANT: Yaves R. Laroche, Laurent S. Jespers,
APPLICANT: Yaves R. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 57.7%; Score 15; DB 2; Length 10; Best Local Similarity 100.0%; Pred. No. 1.9e+03; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Xaa in locations 1 to 3 and CHER INFORMATION: locations 5 to 10 is an amino OTHER INFORMATION: acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: BACAGE
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,399
FILING DATE: Unne 5, 1995
CLASSIFTCATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/26,110
FILING DATE: OCCODER 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/270
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION STORMATION:
TELESHONE: (213) 489-160
TELEFAK: 67-3510
INFORMATION FOR SEQ ID NO: 271:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                      REGISTRATION NUMBER: 30,158
REPRENCE/CDOCKET WINBER: 213/270
RELECHONE: (213) 489-1600
TELEPRA: (213) 955-0440
TELER: 67-3510
INFORMATION FOR SEQ ID NO: 222:
SEQUENC: G7-3510
INFORMATION FOR SEQ ID NO: 222:
SEQUENC: G7-3510
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 CXXXXXX 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXXXXXX 7
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Fatent No. 5866543
Fatent S. Jeansens, Marc J. Lauwereys, APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys, APPLICANT: Pater W. Bergum
Fatent Normanner Pater W. Bergum
Fatent OF INVENTION: NUMATODE-EXTRACTED ANTICOAGULANT
FILLE OF INVENTION: PROTEIN
FILLE OF INVENTION: PROTEIN
FILLE OF INVENTION: REAGE
FORESPONDENCE ADDRESS:
FOREST: 633 West Fifth Street
FIRET: Suite 4700
FIRET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 57.7%; Score 15; DB 2; Length 10; Best Local Similarity 100.0%; Pred. No. 1.9e+03; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Xaa in locations 1 to 3 and OTHER INFORMATION: locations 5 to 10 is an amino OTHER INFORMATION: acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 18 Compatible
COMPUTER: BM Compatible
COMPUTER: BM Compatible
COMPUTER: BM Compatible
COMPUTER: USV COMPATIBLE
CLASSIFICATION NUMBER: 08/326,110
FILLING DATE: OCCOODER 18, 1994
ATTORNEY/AGENT INFORMATION:
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,399
FILING DATE: June 5, 1995
CLASSIFICATION: S, 1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNBER: 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANDE L.
REGISTRATION NUMBER: 213/270
TELECANICAL TON INFORMATION:
TELECHONE: (213) 489-1600
TELECHONE: (213) 955-0440
TELECAN: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acco
TOPOLOGY: linear
FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 67
US-08-486-399-222
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Indels

Pred. No. 1.9e+03; Mismatches 0;

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100.0%;
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Best Local Similarity 100.
Matches, 7; Conservative
Best Local Similarity 100. Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CXXXXXX 7
                                                                                                                     4 CXXXXXX 10
                                                                        1 CXXXXXX 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-461-965-145
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US-08-461-965-145
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                                                                                                                                                                                                                             Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
MUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                        Query Match 57.7%; Score 15; DB 2; Length 10, Best Local Similarity 100.0%; Pred. No. 1.9e+03; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xaa in locations 1 to 3 and locations 5 to 10 is an amino acid.
                                                                                                        OTHER INFORMATION: Xaa in locations 1 to 3 and 7 OTHER INFORMATION: locations 5 to 10 is an amino OTHER INFORMATION: acid.
US-08-486-399-271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY AGENT INPORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30.158
REFERENCE/DOCKET NUMBER: 213/270
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 325:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 69
US-08-486-399-325
Sequence 325, Application US/08486399
Patent No. 5866543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700 STREET: Suite 4700 STREET: Los Angeles STATE: California COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: internal fragment FEATURE:
                                 TOPOLOGY: linear FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inear
                                                                                                                                                                                                                                                                                                                                                                            4 CXXXXXX 10
               amino acid
                                                                                                                                                                                                                                                                                                                             1 CXXXXXX 7
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US-08-461955.148

Sequence 145, Application Us/08461965

Parenn No. 20700300

GRANDALCANT: Vers. R. Lancoche, Lauvent S. Jespecs, Application Us/08-461965, Application Us/08-69-461969, Applicant: Octobe Lauvent S. Jespecs, Application US/08461965

Jespecs, Applicant: Octobe Lauvent US-0861965

Jespecs, Applicant: Octobe Lauvent US-0861965
```

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US-08-271
US-08-461-965-271
US-08-461-965-271
Sequence 271, Application US/08461965
Fatent No. 5972098
GENERAL INFORMATION:
APPLICANT: Goorge P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Peter W. Bergum
TILLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TILLE OF INVENTION: ALYON
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: Callfornia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.7%; Score 15; DB 2; Length 10; 100.0%; Pred. No. 1.9e+03; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTHER INFORMATION: Xaa in locations 1 to 3 and OTHER INFORMATION: locations 5 to 10 is an amino OTHER INFORMATION: acid.

US-08-461-965-222
                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: 1EM Compatible
COMPATIBLE
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
RECISTRATION NUMBER: 210/243
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 222:
COMPUTER: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 10 amino acids
amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fit!
STREET: Guite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 CXXXXXX 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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0
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
GEORGE P. Vlasuk, Patric H. Stanssens,
APPLICANT: George P. Vlasuk, Patric H. Lauwereys,
APPLICANT: Yors R. Laroche. Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: G31 West Fifth Street
STREET: Suite 4700
CITY: LOS Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.7%; Score 15; DB 2; Length 10;
100.0%; Pred. No. 1.9e+03;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 222, Application US/08461965

Patent No. 5872098

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: George P. Vlasuk, Patric H. Stanssens,

APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,

APPLICANT: Yors R. Laroche, Laurent S. Jespers,

APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,

APPLICANT: Peter W. Bergum

TITLE OF INVENTION: NEWATOBE-EXTRACTED ANTICOAGULANT

TITLE OF INVENTION: PROTEIN

TITLE OF SEQUENCES: 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Xaa in locations 1 to 3 and CHER INFORMATION: locations 5 to 10 is an amino OTHER INFORMATION: acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3 torage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,965
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: OCLOBE: 18, 1994
ATTORNEY/AGENT INFORMATION:
RECIPERATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 210/243
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: 7-3510
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 10 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CXXXXXX 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CXXXXXX 7
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US-08-461-965-222
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Query Match 57.7%; Score 15; DB 2; Length 10; Best Local Similarity 100.0%; Pred. No. 1.9e+03; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Xaa in locations 1 to 3 and ; OTHER INFORMATION: locations 5 to 10 is an amino OTHER INFORMATION: acid.
US-08-461-965-325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GEORGE P. VLASUK; PATRICK ERIC
APPLICANT: LIVEN MESSENS; JORIS HILDA
APPLICANT: LIVEN MESSENS; MAC JOZEF
APPLICANT: LAUWERENS; YVES RENE LAROCHE;
APPLICANT: LAUWENT STEPHANE JESPERS; and
APPLICANT: YANNICK GEORGES JOZEF
APPLICANT: YANNICK GEORGES JOZEF
APPLICANT: GANSEMANS
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTI-
TITLE OF INVENTION: OCAGULANT PROTEIN
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: LYON & LYON
STREET: 633 West Fifth Street
STREET: 634 West Fifth Street
STREET: California
COINTRY: U.S.A.
ZIP: 90071
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 8 torage
COMPUTER: IBM COMPATIBLE
OFFRATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FARISE Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/326,110A
FILING DATE: 18 OCTOBER 1994
CLASSIFCATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
PILLING DATE: OCCUMATION.

ATTORNEY/AGENT INFORMATION.

NAME: BIGGS, SUZANNE L.

REGISTRATION NUMBER: 30,158

REFERENCE/DOCKET NUMBER: 210/243

TELEPHONE: (213) 489-1600

TELEPHONE: (213) 955-0440

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 325:
SEQUENCE CHARACTERISTICS:
ELENGTH: 10 amino acid

TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208/290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-326-110A-76
; Sequence 76, Application US/08326110A
; Patent No. 5945275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 208/3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 CXXXXXX 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CXXXXXX 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 74

US-06-461-965-325

i Sequence 325, Application US/08461965

i Patent No. 5872098

i GENERAL INFORMATION:

APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Yors R. Laroche, Laurent S. Jespers,
APPLICANT: Yors R. Laroche, Laurent S. Jespers,
APPLICANT: Your M. Laroche, Laurent S. Jespers,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
CONNTRY: US.A.
ZIP: PETER DEST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.7%; Score 15; DB 2; Length 10; 100.0%; Pred. No. 1.9e+03; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Xaa in locations 1 to 3 and 1 CTHER INFORMATION: locations 5 to 10 is an amino US-08-461-965-271
             MEDIUM TYPE: storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
CORTWARE: Word Berfect 5.1
SCHWARE: Word Berfect 5.1
APPLICATION VUMBER: US/08/461,965
FILING DATE: US/08/461,10
FILING DATE: US/08/461,10
FILING DATE: US/08/461,10
FILING DATE: US/08/461,10
FRESPRATION NUMBER: 30,188
FREFRENCE/DOCKET NUMBER: 210/243
FELECHMONICATION INMERE: 210/243
FELEPHONE: (213) 965-6440
TELEFAX: (213) 955-6440
TELEFX: 67-3510
INFORMATION FOR SEQ ID NO: 271:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acids
TYPE: amino acid
TYPE: unance internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,965
FILING DATE: June 5, 1995
CLASSIPICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 90071
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
FRAGMENT TYPE: internal fragment
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CXXXXXX 7
```

Gaps

```
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TYPE: amino acids
TYPE: amino a
```

Search completed: May 4, 2004, 06:53:03 Job time: 23 secs

1 CXXXXXX 7 | | | | | | | | | 4 CXXXXXX 10

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

May 4, 2004, 06:53:08; Search time 41 Seconds (without alignments) 67.607 Million cell updates/sec Run on:

US-10-046-922-33 26 1 CXXXXXXX 10 Title: Perfect score: Sequence:

PAM150XX Gapop 10.0 , Gapext 0.5 Scoring table:

1138120 segs, 277189581 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 10 Maximum DB seq length: 10

Post-processing: Minimum Match 50% Maximum Match 100% Listing first 100 summaries

Database :

Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/USO7\_PUBCOMB.pep:\*
2: /cgn2\_6/ptodata/1/pubpaa/PUSO\*MW PUBL.pep:\*
3: /cgn2\_6/ptodata/1/pubpaa/PUSO\*MW PUBL.pep:\*
4: /cgn2\_6/ptodata/1/pubpaa/USO6\_PUBCOMB.pep:\*
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6: /cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*
7/cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*
8: /cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*
9: /cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*
11: /cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*
12: /cgn2\_6/ptodata/1/pubpaa/USO9\_PUBCOMB.pep:\*
13: /cgn2\_6/ptodata/1/pubpaa/USO9\_PUBCOMB.pep:\*
14: /cgn2\_6/ptodata/1/pubpaa/USO9\_PUBCOMB.pep:\*
15: /cgn2\_6/ptodata/1/pubpaa/USO9\_PUBCOMB.pep:\*
16: /cgn2\_6/ptodata/1/pubpaa/USO0\_PUBCOMB.pep:\*
17: /cgn2\_6/ptodata/1/pubpaa/USO0\_PUBCOMB.pep:\*
18: /cgn2\_6/ptodata/1/pubpaa/USO0\_PUBCOMB.pep:\*
19: /cgn2\_6/ptodata/1/pubpaa/USO0\_PUBCOMB.pep:\*
11: /cgn2\_6/ptodata/1/pubpaa/USO0\_PUBCOMB.pep:\*
11: /cgn2\_6/ptodata/1/pubpaa/USO0\_PUBCOMB.pep:\*
11: /cgn2\_6/ptodata/1/pubpaa/USO0\_PUBCOMB.pep:\*
11: /cgn2\_6/ptodata/1/pubpaa/USO0\_PUBCOMB.pep:\*
11: /cgn2\_6/ptodata/1/pubpaa/USO0\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Sequence 11, Appl	Sequence 11, Appl	Sequence 3, Appli	Sequence 110, App	Sequence 33, Appl	Sequence 133, App	Sequence 21, Appl	Sequence 101, App	Sequence 42, Appl	Sequence 200, App	Sequence 249, App	Sequence 299, App	Sequence 352, App	Sequence 39, Appl	GENERAL INFORMA
ΠD	US-09-932-613-11	US-09-932-322-11	US-09-825-517A-3	US-09-825-517A-110	US-10-046-922-33	US-10-094-401-133	US-10-396-073-21	US-10-462-262-101	US-09-364-597A-42	US-09-498-272-200	US-09-498-272-249	US-09-498-272-299	US-09-498-272-352	US-09-922-227-39	US-09-498-272-145
	10	10	11	디	13	14	15	15	σ	10	10	10	10	12	10
Query Match Length DB	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	65.4	65.4	65.4	65.4	65.4	65.4	57.7
Score	26	56	26	26	26	56	26	26	17	17	17	17	17	17	15
Result No.	п	7	m	4	Ŋ	9	7	80	6	10	11	12	13	14	15

Sequence 173, App Sequence 222, App Sequence 271, App Sequence 325, App	4,17,14 4,47,1	19, AI 67, 1	Sequence 19, Appl Sequence 19, Appl Sequence 67, Appl	Sequence 18, Appl Sequence 26, Appl Sequence 75, Appl	Sequence 78, Appl Sequence 19, Appl Sequence 21, Appl Sequence 19, Appl Sequence 19, Appl
0 US-09-498-272-173 0 US-09-498-272-222 0 US-09-498-272-21 0 US-09-498-272-325	US-09-861-101- US-10-297-229- US-10-013-815-	Þ	0 US-09-893-878-19 1 US-09-896-095-19 2 US-10-271-869-67	4 US-10-098-093-18 4 US-10-098-093-26 4 US-10-013-815-75	4 US-10-013-815-78 5 US-10-126-685-19 5 US-10-186-229-21 5 US-10-126-544-19 6 US-10-126-544-19
100 100 100 100 100 100 100 100 100 100		10 10 10 10 10	222	202	
15 57.7 15 57.7 15 57.7 15 57.7	15 57.7 15 57.7 14 53.8	14 53.8 13 50.0 13 50.0	13 50.0 7 13 50.0 13 50.0	13 50.0 13 50.0 13 50.0	13 50.0 13 50.0 13 50.0 13 50.0
777 777 84	8888	C) C) C)	22.2	10 0 E	w w w w w

## ALIGNMENTS

Inc. PTIDES AND METHODS BASED THEREON -025.1 US	//932,613 Dolypeptide	His, Ile, Leu, Lys, Met, Phe, or Thr;	Leu, Met, Phe, Pro, Trp, or Tyr; Leu, or Ser (preferably Asp);	Asp,	Asn, or red Met, Pro, Se	Asn, Gly, His, Lys, Ser, or Tyr; Asn, Gln, Leu, Met, Ser, Trp, Tyr, or Val;
RESULT 1 US-09-932-613-11 Sequence 11, Application US/09932613 Publication No. US20030091565A1 GENERAL INFORMATION: APPLICANT: Human Genome Sciences, Inc. APPLICANT: Beltzer, James P. APPLICANT: Potter, M. Daniel APPLICANT: Fleming, Tony J. TITLE OF INVENTION: BINDING POLYPEPTIDES, FILE REFERENCE: Dyx-025.1 PCT; DXX-025.1	CURRENT APPLICATION NUMBER: US/09/93 CURRENT FILING DATE: 2001-08-17 NUMBER OF SEQ ID NOS: 458 SOFTWARE: Patentin version 3.1 SEQ ID NO 11 ENGTH: 10 TYPE: PRT ORGANISM: Artificial Sequence FRATURE: PRT ORGANISM: Artificial Sequence	s Asp, G]	OTHER INFORMATION: X3 is His, Ile, NAME/KEY: MISC FEATURE LOCATION: (4)(4) OTHER INFORMATION: X4 is Asp, His, NAME/KEY: MISC_FEATURE	is Ala, ro);	) OTHER INFORMATION: X6 IS AIR, AIG, NAME/KEY: MISC_FEATURE ) COCATION: (7)(7) ) OTHER INFORMATION: X7 is Ile, Leu, NAME/KEY: MISC_FEATURE	COTHER INFORMATION: X8 is Ala, Arg, NAME/KEY: MISC_FEATURE LOCATION: (9)(9) COTHER INFORMATION: X9 is Ala, Arg,

```
Query Match 100.0%; Score 26; DB 11; Length 10; Best Local Similarity 100.0%; Pred. No. 0.35; Matches 10; Conservative 0; Mismatches 0; Indels
                   APPLICANT: Rondon, Issac J
APPLICANT: Rondon, Issac J
APPLICANT: Ladner, Robert C
TITLE OF INVENTION: BINDING PEPTIDES FOR CARCINOEMBRYONIC
TITLE OF INVENTION: ANTIGEN (CEA)
FILE REFERENCE: DXX-016.1 (3421.1065-001)
CURRENT APPLICATION NUMBER: US/09/825.517A
CURRENT FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US 09/541,345
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 151
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 110, Application US/09825517A
Publication No. US20030203415A1
GENERAL INFORMATION:
APPLICANT: Rondon, ISSAC J
APPLICANT: Rondon, ISSAC J
APPLICANT: LAGINER, Robert C
TITLE OF INVENTION: BINDING PEPTIDES FOR CARCINOEMBRYONIC
FILE REFERENCE: DYX. 0.16.1 (3421.1005-001)
CURRENT APPLICATION NUMBER: US/09/825,517A
CURRENT FILING DATE: 2003-03-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) NAME/KEY: VARIANT

LOCATION: (9) ...(9)

) OTHER INFORMATION: Xaa is Ala, Gly, His, Phe, Thr or Val

US-09-825-517A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 4
OTHER INFORMATION: Xaa is Asp, Gly, Ile, Lys, Phe or Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 6
OTHER INFORMATION: Xaa is Arg, Asn, Asp, Glu or Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KRE: VARIANT
NAME/KRE: VARIANT
OCATION: 5
OTHER INFORMATION: Xaa is Ala, Gln, Gly, Ly8 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: VARIANT
LOCATION: 3
OTHER INFORMATION: Xaa is Asn, Leu, Met or Phe
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
OTHER INFORMATION: CEA binding loop
FEATURE:
NAME/KEY: VARIANT
LOCATION: 2
OTHER INFORMATION: Xaa is Asn, Glu or Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (8)...(8)
OTHER INFORMATION: Xaa is Ala, Trp or Tyr
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: VARIANT
LOCATION: (7)...(7)
OTHER INFORMATION: Xaa is Gln, Gly
                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CXXXXXXXC 10
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BENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-825-517A-110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OCHER INFORMATION: X5 is Ala, Arg, Asp, Glu, Leu, Phe, Pro, or Thr (preferably Glu of OTHER INFORMATION: r Pro);

NAME/EXEX INFORMATION: r Pro);

NAME/EXEX: MISC FEATURE
LOCATION: (6)...(6)

OTHER INFORMATION: X6 is Ala, Arg, Asn, or Leu (preferably Leu);

NAME/EXEX: MISC FEATURE
LOCATION: (7)...(7)

OTHER INFORMATION: X7 is Ile, Leu, Met, Pro, Ser, or Thr (preferably Thr);

NAME/EXEX: MISC FEATURE
LOCATION: (8)...(9)
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dyax Corp.
APPLICANT: Dyax Corp.
APPLICANT: Dotter, James P.
APPLICANT: Dotter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Ladner, Robert Charles
APPLICANT: Ladner, Robert Charles
TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (BLyS)
FILE REPERENCE: DYA-018.1 PCT; DYX-018.1 US
CURRENT APPLICATION NUMBER: US/09/932,322
CURRENT FILING DATE: 2001-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (9) _ (9) _ 0 THE TAGE AND GIN, Leu, Met, Ser, Trp, Tyr, or Val; US-09-932-322-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: MIGG FEATURE
LOCATION: (2).-(2)
TOTHER INFORMATION: X2 is Asp, Gln, His, Ile, Leu, Lys, Met, Phe, or Thr;
NAME/KEY: MIGG FEATURE
LOCATION: (3).-(3)
TOTHER INFORMATION: X3 is His, Ile, Leu, Met, Phe, Pro, Trp, or Tyr;
NAME/KEY: MIGG FEATURE
LOCATION: (4).-(4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (8). (8) (8) OTHER INFORMATION: X8 is Ala, Arg, Asn, Gly, His, Lys, Ser, or Tyr; NAME/KEY: MISC. FRATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ION: (4). (4)
INFORMATION: X4 is Asp, His, Leu, or Ser (preferably Asp);
KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                               Query Match
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-02-825-517A-3
Sequence 3, Application US/09825517A
Publication No. US20030203415A1
                                                                                                                                                                                                                                                                                         RESULT 2
US-09-932-322-11
Sequence 11, Application US/09932322; Publication No. US20030194743A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 458
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
EBNOTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CXXXXXXXX 10
                                                                                                                                                           1 CXXXXXXXX 10
                                                                                                                                                                                                           1 CXXXXXXXX 10
     US-09-932-613-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ПЪ
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Gaps

.. 0

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Gaps
                                                                                                                                                                                                                                                           LOCATION: (4)...(4)
OTHER INFORMATION: X is tryptophan or a conservative substitution
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (7)...(7)
OTHER INFORMATION: X is isoleucine or a conservative substitution NAME/KEY: SITE
LOCATION: (8)...(8)
OTHER INFORMATION: X is tryptophan or a conservative substitution
                                                                                                                                                                                                                                                                                                                                                                                                                                 is threonine or a conservative substitution
                                                                                                                                                                                 LOCATION: (3)..(3)
OTHER INFORMATION: X is tyrosine or a conservative substitution NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) LOCATION: (9)..(9) ; OTHER INFORMATION: X is glycine or a conservative substitution US-10-046-922-33
                                                                                                                                                                                                                                                                                                                                                          is leucine or a conservative substitution
                                                                                                            LOCATION: (2)...(2)
OTHER INFORMATION: X is glycine or a conservative substitution AAMZ/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 26; DB 13; Length 10; 100.0%; Pred. No. 0.35; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Sato, Aaron K.
APPLICANT: Lay, Arthur C.
APPLICANT: Ley, Arthur C.
APPLICANT: Ley, Arthur C.
TITLE OF INVENTION: SERUM ALBUMIN BINDING MOIETIES
FILE REFERENCE: DYX-026.2 PCT; DYX-026.2 US
CURRENT APPLICATION NUMBER: US/10/094,401
CURRENT FILING DATE: 2002-03-08
PRIOR PILING DATE: 2001-03-09
PRIOR PILING DATE: 2001-03-09
PRIOR PILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 271
SOPTWARE: Patentin version 3.1
SEQ ID NO 133
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHER INFORMATION: albumin binding peptide NAME/KEY: MISC_FEATURE LOCATION: (2)...(2) OTHER INFORMATION: Gln, Glu, Phe, or Met NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (3)...(3)
OTHER INFORMATION: Asp, Pro, or Thr
NAME/KEY: MISC FEATURE
LOCATION: (4)...(4)...(4)
OTHER INFORMATION: Ile, Ser, or Trp
NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-094-401-133
Sequence 133, Application US/10094401
Publication No. US20030069395A1
GENERAL INFORMATION:
APPLICANT: DYAX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                     ORGANISM: isolated peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                               LOCATION: (5)...(5)
OTHER INFORMATION: X 1
NAME/KEY: SITE
LOCATION: (6)..(6)
OTHER INFORMATION: X 1
NAME/KEY: SITE
                                                                                       NAME/KEY: SITE
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; OTHER INFORMATION: X is Phe, Thr, Met, Ser, Ala, Asn, Val, His, Ile,
; OTHER INFORMATION: Pro, Trp, Tyr, Gly, Leu or Glu
US-09-825-517A-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 6
OTHER INFORMATION: X is Asn, Pro, Phe, Gly, Asp, Ala, Ser, Glu, Gln,
OTHER INFORMATION: Trp, His, Arg, Met, Val or Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: VARIANT
LOCATION: 4
OTHER INFORMATION: X is Phe, Leu, Asp, Glu, Ala, Ile, Lys, Asn, Ser,
OTHER INFORMATION: Val, Trp, Tyr, Gly or Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: VARIANT
LOCATION: 5
OTHER INFORMATION: X is Lys, Phe, Asp, Gly, Leu, Asn, Trp, Ala, Gln
OTHER INFORMATION: or Thr
                                                                                                                                                                                                                                                                                                                                                            FRATURE:
NAME/KEY: VARIANT
LOCATION: 3
OTHER INFORMATION: X is Leu, Phe, Tyr, Trp, Val, Met, Ile or Asn
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
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APPLICANT: Kolvunen, Erkki
APPLICANT: Kubo, Halime
TITLE OF INVENION: VEGER-3 INHIBITOR MATERIALS AND METHODS
FILE REFERENCE: 28967/37084A
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SEQ ID NOS 33
LENGTH: 10
                                                                                                                                                                                                                                   OTHER INFORMATION: Synthetic 16-mer microprotein analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (7)...(7)
OTHER INFORMATION: X is Gln, Lys, Leu or Gly
                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: X is Asn, Glu, Asp or Met
PRIOR APPLICATION NUMBER: US 09/541,345
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 151
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 110
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (8)...(8)
OTHER INFORMATION: X is Tyr, Trp or Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 33, Application US/10046922
Publication No. US20020164667A1
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: VARIANT
LOCATION: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: VARIANT
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FEATURE:

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Gaps
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100.0%; Score 26; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 10; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
MCRANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: example of serum albumin-binding agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (9)...(0)
CTHER INFORMATION: Xaa = Asp, Gly, Phe, or Trp
US-10-462-262-101
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LOCATION: (8)...(0)
OTHER INFORMATION: Xaa = Arg, Met, Phe, or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: VARIANT
LOCATION: 5
OTHER INFORMATION: Xaa = His, Met, Phe or Pro
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 101, Application US/10462262
Sequence 101, Application US/10462262
PUDLication No. US20040009534A1
GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
TILLE OF INVENTION: PROTEIN ANALYSIS
FILE REFERENCE: 10280-05201
CURRENT APPLICATION NUMBER: US/10/462,262
CURRENT PILING DATE: 2003-06-16
PRIOR FILING DATE: 2003-06-14
NUMBER OF SEQ ID NOS: 430
SOFTWARE: FastSEQ for Windows Version 4.0
SSOTUMARE: PASTSEQ for Windows Version 4.0
SENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: VARIANT
LOCATION: 2
OTHER INFORWATION: Xaa = Gln, Glu, Phe, or
FEATURE:
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TOTHER INFORMATION: Xaa = Asn, Leu, or Thr
FEATURE:
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 3
OTHER INFORMATION: Xaa = Asp, Pro, or Thr
FEATURE:
         OTHER INFORMATION: X8 is Leu, Pro, or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (7)...(0)
OTHER INFORMATION: Xaa = Arg, Asn, His,
PEATURE:
                                  FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (9)...(9)

OTHER INFORMATION: X9 is Trp or Tyr
US-10-396-073-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 4
OTHER INFORMATION: Xaa = Ile, Ser,
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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Best Local Similarity
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US-10-462-262-101
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OTHER INFORMATION: fibrinogen binding polypeptide
FEATURE:

NAME/KEY: MISC_FEATURE

LOCATION: (2)...(2)

OTHER INFORMATION: XZ is Asn, Met, or Ser

FEATURE:

NAME/KEY: MISC_FEATURE

LOCATION: (3)...(3)

OTHER INFORMATION: XZ is Ala or Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21, Application US/10396073
Publication No. US2003020733041
GENERAL INFORMATION:
APPLICANT: Wescott, Charles R.
APPLICANT: Sato, Aaron K.
TITLE OF INVENTION: PIBRINGGEN BINDING MOIETIES
FILE REPRENCE: DVX.036.1 PCT; DXX-036.1 US
CURRENT FILING DATE: 2003-03-25
FRICA RPLICATION NUMBER: US 60/367,645
FRICA RPLICATION NUMBER: US 60/367,645
NUMBER OF SEQ ID NOS: 48
SEQ ILING DATE: 2002-03-26
SEQ IL NOS: 48
SEQ IL NOS: 21
LENGTH: 10
LOCATION: (5)...(5)

OTHER INFORMATION: His, Met, Phe or Pro
NAME/KEY: MISC_FEATURE
COCATION: (6)...(6)
OTHER INFORMATION: Asn, Leu, or Thr
NAME/KEY: MISC_FEATURE
COCATION: (7)...(7)
OTHER INFORMATION: Arg, Asn, His, or Thr
NAME/KEY: MISC_FEATURE
COCATION: (8)...(8)
OTHER INFORMATION: Arg, Met, Phe, or Tyr
NAME/KEY: MISC_FEATURE
COCATION: (9)...(9)
COCATION: (9)...(9)
COCATION: (9)...(9)
COCATION: (9)...(9)
COCATION: Asp, Gly, Phe, or Trp
US-10-094-401-133
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OTHER INFORMATION: X6 is Ile, Met, or Tyr
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (7)...(7)
OTHER INFORMATION: X7 is Ala, His, or Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (5). (5)
OTHER INFORMATION: X5 is Pro, Thr, or Trp
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LOCATION: (4). (4). (4)
OTHER INFORMATION: X4 is Arg, Asn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CXXXXXXXX 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: artificial
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Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
INHIBITORS AND ANTICOAGULANT
PROTEIN
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Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/498,272
PILING DATE: 04-Fb-200
PRIOR APPLICATION NUMBER: PCT/US95/13231
PILING DATE: OCTOBE 17, 1995
APPLICATION NUMBER: 08/466,399
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/466,397
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/46,965
FILING DATE: Unne 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: OCTOBER: 08/461,965
FILING DATE: OCTOBER: 08/36,110
FILING DATE: OCTOBER: 08/36,110
FILING DATE: OCTOBER: 08/36,110
APPLICATION NUMBER: 08/36,110
FILING DATE: OCTOBER: 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REFERENCE/DOCKET NUMBER: 216/270
TELEPRAN: (213) 955-0440
                                                                                                                                                                                                                                                                                                 ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Vlasuk, George Phillip
Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 200: US-09-498-272-200
                                                                                                            NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
FRAGMENT TYPE: internal fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 67-3510 INFORMATION FOR SEQ ID NO: 200:
                                                                                                                                                                                                                               CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-498-272-249
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Sequence 42, Application US/09364597A
Patent No. US20020103130A1
GENERAL INFORMATION:
APPLICANT: Rucelant, Erkki
APPLICANT: Koivunen, Erkki
TITLE OF INVENTION: No. US20020103130A1e1 Integrin-Binding Peptides
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
  Gaps
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  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DUS/MS-DUS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/364,597A
FILING DATE: 30-JUL-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/266,861
FILING DATE: 04-NUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAMPADELL, CALLYON
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 3419
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (858) 535-9001
TELEFRAX: (858) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 200, Application US/09498272
Publication No. US20030113890A1
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yannick Georges Jozef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17; DB 9; Le
; Pred. No. 3.8e+02;
0; Mismatches 0;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 100.0%;
Matches 9; Conservative 0
10; Conservative
                                               1 CXXXXXXXC 10
                                                                                          1 CXXXXXXXX 10
                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 4370 La Jo
CITY: San Diego
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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US-09-498-272-200
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  Matches
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Gaps

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Xaa in locations 2 to 10 is an
                                                                                            Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Moyle, Matthew
Bergum, Peter W.
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,272
FILING DATE: 04-Feb-200
PRIOR APPLICATION NUMBER: PCT/US95/13231
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/361,10
FILING DATE: June 5, 1995
ATTORNEY/AGENT INROBER: 08/326,110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFREENCE/DOCKET NUMBER: 216/270
TELECOMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; SEQUENCE DESCRIPTION: SEQ ID NO: 299:
US-09-498-272-299
                                                                       Messens, Joris Hilda Liever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGIH: 10 amino acids
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INFORMATION FOR SEQ ID NO: 299:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: LyON & Ly
STREET: 633 West Fif
State 64700
                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                  Stanssens,
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  GENERAL INFORMATION:
APPLICANT: Vlas
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                                                                                                                         Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.4%; Score 17; DB 10; Length 10;
100.0%; Pred. No. 3.8e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                         INHIBITORS AND ANTICOAGULAN'
Lauwereys, Marc Josef
Laroche, Yves Rene
Despers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Moyle, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION TOWNER: US/09/498,272
FILING DATE: 04-Feb-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/36,110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 216/270 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid.

SEQUENCE DESCRIPTION: SEQ ID NO: 249:
US-09-498-272-249
                                                                                                                                                                                                                                                                   ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 299, Application US/09498272; Publication No. US20030113890A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 249:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 storage
                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Conservative
                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-09-498-272-299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                  APPLICANT: Rouglahti, Erkki
APPLICANT: Rusalahii, Renata
TITLE OF INVENTION: Method of Identifying Molecules That
Home to a Selected Organ In Vivo
                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Johla Village Drive, Suite 700

CITY: San Diego

STATE: California

COMPUTER: Eablable FORM:

MEDTIUM TYPE: FLORPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Ralease #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/922,227

FILING DATE: 11-SEP-1997

APPLICATION NUMBER: US 08/813,273

FILING DATE: 11-MAR-1997

APPLICATION NUMBER: US 08/813,273

FILING DATE: 11-MAR-1997

APPLICATION NUMBER: US 08/813,273

FILING DATE: 12-MAY-1997

APPLICATION NUMBER: US 08/82,855

FILING DATE: 23-MAY-1997

APPLICATION NUMBER: US 08/827,906

FILING DATE: 12-MAY-1999

APPLICATION NUMBER: US 09/227,906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
65.4%; Score 17; DB 12; I
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-09-498-272-145
, GENERAL INFORMATION:
, APPLICANT: Vlasuk, George Phillip
Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
Messens, Marc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET WUMBER: P-LJ 4859
TELECOMUNICATION INFORMATION:
TELEPHONE: (619) 535-9949
TELEFAX: (619) 535-9949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                 Sequence 39, Application US/09922227 Publication No. US20040071689A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CXXXXXXXX 9
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                                                                      RESULT 14
US-09-922-227-39
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                                                                                         APPLICANT: Usuk, George Phillip
APPLICANT: Stanseens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Moyle, Matthew
Bergum, Peter W
IITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xaa in locations 2 to 10 is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.4%; Score 17; DB 10; Length 10; 100.0%; Pred. No. 3.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM COMPACTE, 1134 FD.

BECTAGE
COMPUTER: IBM COMPACTED
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PARÍECT 5.1
CURRAY APPLICATION DATA:
APPLICATION NUMBER: US/09/498,272
FILING DATE: 04-Feb-2000
PRIOR APPLICATION NUMBER: PCT/US95/13231
FILING DATE: Cotcober 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: Gotcober 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
SEQUENCE DESCRIPTION: SEQ ID NO: 352:
US-09-498-272-352
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear FRAGMENT TYPE: internal fragment
JS-09-498-272-352; Sequence 352, Application US/09498272; Publication No. US20030113890A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 10 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 352:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: LOS Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE
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Gaps
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S7.7%; Score 15; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 10 is an amino
                                                                                                                                                                                                                                                                                          COMPUTER: 15% CARACLE, 113 ::...

STORAGE
COMPUTER: 15M COMPATIBLE
OPERATING SYSTEM: 15M P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,272
FILING DATE: 04-FEb.2000
FILING DATE: 04-FEb.2000
FILING DATE: 04-FEb.395
APPLICATION NUMBER: 08/466,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/466,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/361,10
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/361,10
FILING DATE: JUNE 5, 1994
ATTORNEY/ABGNT INFORMATION:
                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Vlasuk, George Phillip
Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Jespers, Laurent Stephane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BIGGS, SUZANNE I.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; SEQUENCE DESCRIPTION: SEQ ID NO: 173; US-09-498-272-173
                        NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPATA: (213) 489-1600
TELEPAT: (213) 955-0440
TELEAT: 67-3510
INPORMATION FOR SEQ ID NO: 173:
SBQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 222, Application US/09498272
Publication No. US20030113890A1
GENERAL INFORMATION:
                                                                                                                                                 CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 CXXXXXX 10
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US-09-498-272-222
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US-09-488-272-173
US-09-488-272-173
Sequence 173, Application US/09498272
Publication No. US20030113890A1
Sequence 173, Application US/09498272
Sequence 173, Application No. US20030113890A1
Seanseans, Patrick Eric Hugo
Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
Laroche, Yves Rene
Gansemans, Yannick Georges Jozef
Gansemans, Yannick Georges Jozef
Myle, Matchew
Bergum, Peter N
Bergum, Peter N
ITILE OF INVENTION: NEWATODE-EXTRACTED SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                              Bergum, Peter W.

TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
INVENTION: LIMIBITORS AND ANTICOAGULANT
PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.7%; Score 15; DB 10; Length 10; 100.0%; Pred. No. 1.8e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           CCMPUTER: IBM COMPATIBLE

OPERATING SYSTEM: IBM C. DOS 5.0
SOFTWARE: WOLD BAFE:

CURRENT APPLICATION DATE:

PRIOR APPLICATION DATE:

APPLICATION NUMBER: US/09/498,272
FILING DATE: 04-Feb-200

PRIOR APPLICATION NUMBER: PCT/US95/13231
FILING DATE: OLIDER 17, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/466,365
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/466,365
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/466,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 30,159
APPLICATION NUMBER: 30,159
APPLICATION NUMBER: 30,159
APPLICATION NUMBER: 30,159
APPLICATION NUMBER: 30,160
FILING DATE: ABSTANION TORDANTION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION: SEQ ID NO: 145:
US-09-498-272-145
Gansemans, Yannick Georges Jozef
Moyle, Matthew
                                                                                                                                                                                                                                                                                                                           COUNTRY SUDDIT COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSES: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                    NUMBER OF SEQUENCES: 356
                                                                                                                                                                                                                                                                       CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.v.
....hes 7; Conservative
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Gaps
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llarity 100.0%; Pred. No. 1.8e+03;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                              Bergum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 10 is an amino
                                        Lauwerrys, Marc Josef
Laroche, Yves Rene
Laspers, Laurent Stephane
Gansemans, Yannick Georges Jozef
Moyle, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,272
FILING DATE: 04-Feb-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: Ottober 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: JUME 5, 1995
APPLICATION NUMBER: 08/466,380
FILING DATE: JUME 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: JUME 5, 1995
APPLICATION NUMBER: 08/326 110
FILING DATE: OCCODER 18, 1994
ATTORNEY/ABGNT INCORDATION:
                                                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECONMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELER: 67-3510
INFORMATION FOR SEQ ID NO: 271:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 aming acids
Stanssens, Patrick Eric Hugo
                         Messens, Joris Hilda Lieven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acid.
SEQUENCE DESCRIPTION: SEQ ID NO: 271:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                        PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 storage
                                                                                                                                                                                                                                                                                                             ADDRESSEE: Lyon & I
STREET: 633 West Fi
Suite 4700
                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     음
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                                              DESCRIPTION: DETER W. PETER OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Xaa in locations 1 to 3 and locations 5 to 10 is an amino
     Gansemans, Yannick Georges Jozef
Moyle, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD BELEGET 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,272
FILING DATE: O4-Feb-2000
PRIOR APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/46,965
FILING DATE: October 18, 1994
ATTORNEY'AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 316/270
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; SEQUENCE DESCRIPTION: SEQ ID NO: 222: US-09-498-272-222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 18
US-09-498-272-271
; Sequence 271, Application US/09498272
; Publication No. US20030113890A1
; GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67.3510
INFORMATION FOR SEQ ID NO: 222:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 10 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                       CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 CXXXXXX 10
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; OTHER INFORMATION: "Xaa" stands for either Ala or Thr.; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-861-101-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15; DB 12; Length 10;
Pred. No. 1.8e+03;
0; Mismatches 0; Indels
                                                                                                                                                                                                           SCHWARTZ, ROBERT
DEMAXO, FRANCESCO.
TITLE OF INVENTION: 1GP-1 EXPRESSION SYSTEM AND
METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COBERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/861,101
FILING DATE: 18-May-2001
CLASSIFICATION NUMBER: 08/974,572
FILING DATE: November 19, 1997
APPLICATION NUMBER: 06/031,539
FILING DATE: December 2, 1996
ATTORNEY/AGBNT INFORMATION:
NAME: Warburg, Richard J.
RETERENGE/DOCKET NUMBER: 32,327
REFERENGE/DOCKET NUMBER: 230/185-PCT
TELEPHONE: (213) 955-0440
TELEPAX: (213) 955-0440
TELEPAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
COUNTR: U.S.A.
ZIP. 90071-2066
COMPUTER RRADABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.7%; Sco.
100.0%; Pre
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Publication No. US20030220245A1
GENERAL INFORMATION:
APPLICANT: HUBBELL, Jeffrey A.
                                                                                     RESULT 20
US-09-861-101-6
; Sequence 6, Application US/09861101
; Publication No. US20030018984A1
; GENERAL INFORMATION:
                                                                                                                                                                                         APPLICANT: COLEMAN, MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                 Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 100.
Matches 7; Conservative
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0
57.7%; Score 15; DB 10; Length 10; 100.0%; Pred. No. 1.8e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xaa in locations 1 to 3 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,272
FILING DATE: 04-Feb-200
PRIOR APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/466,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Los Angeles
STATE: California
COUTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: BIGGS, SUZANNE L.
REGISCHATTON VUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; SEQUENCE DESCRIPTION: SEQ ID NO: 325: US-09-498-272-325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Xaa in le locations 5 to 10 is an amino
                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (213) 489-1600
TELEFRAR: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 325:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 7; Conservative
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Gaps

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CXXXXXX 7

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Kent, Rachel Baribault
TITLE OF INVENTION: Directed Evolution of No. US20020150881A1el
Binding Proteins
                                                                                         APPLICANT: Read, Stephanie
APPLICANT: Krag, David
APPLICANT: CAS, David
APPLICANT: Oligino, Lyn
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING GRB7
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING GRB7
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING GRB7
CURRENT APPLICANTON NUMBER: US/10/013,815
CURRENT FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 194
SEQ ID NO 79
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: One Embodiment of General Formula
NAME/KEY: MISC_FEATURE
LOCATION: (2)...(6)
OTHER INFORMATION: Xaa = any amino acid
NAME/KEY: MISC_FEATURE
LOCATION: (8)...(8)
OTHER INFORMATION: Xaa = any amino acid
US-10-013-815-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.8%; Score 14; DB 14; 100.0%; Pred. No. 3.8e+03; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MIDIUM TYPER: Floppy disk
COMPUTER: INPO COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MORDPERFECT 4.2
CURRIT APPLICATION DATA:
REPLICATION NUMBER: US/09/781,988
FILING DATE: 14-Peb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: «UTKNOWN»
PRIOR APPLICATION NUMBER: 07/664,989
FILING DATE: «UTKNOWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guterman, Sonia Kosow
Roberts, Bruce Lindsay
Markland, William
Ley, Arthur Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ladner, Robert Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19, Application US/09781988 Patent No. US20020150881A1 GENERAL INFORMATION:
                         Sequence 79, Application US/10013815 Publication No. US20030105000A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-781-988-19
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APPLICANT: SCHOENWAKERS, Ronald
TITLE OF INVENTION: CONTUGATE ADDITION REACTIONS FOR THE
FILLE OF INVENTION: CONTOLLED DELIVERY OF PHARMACEUTICALLY ACTIVE COMPOUNDS
FILLE REFERENCE: 50154/003002
CURRENT APPLICATION NUMBER: US/10/297,229
CURRENT PILING DATE: 2002-10-02
PRIOR FILLING DATE: 2001-06-04
PRIOR FILLING DATE: 2000-06-02
PRIOR PILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 77
SOFTWARE: FRRESEQ for Windows Version 4.0
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APPLICANT: Krag, David
APPLICANT: Oligino, Lyn
FILLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING GRB7
FILLE REPERRANCE: VO139/7048 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/013,815
PRIOR FILLING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: US 60/245,755
PRIOR FILLNO DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 194
SEQ ID NO 74
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.8%; Score 14; DB 14; Length 10;
100.0%; Pred. No. 3.8e+03;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: One Embodiment of General Formula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

57.7%; Score 15; DB 15; 1

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: VARIANT; LOCATION: (1)...(10); OTHER INFORMATION: Xaa=any amino acid except Cys US-10-297-229-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MISC_FEATURE
COCATION: (3)...(3)
OTHER INFORMATION: Xaa = any amino acid
NAME/KEY: MISC_FEATURE
LOCATION: (5)...(9)
COTHER INFORMATION: Xaa = any amino acid
195-10-013-815-74
                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Based on Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-013-815-74
; Sequence 74, Application US/10013815
; Publication No. US20030105000A1
; PUBLICATION .
; APPLICANT: Perc, Stephanie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                              SEQ ID NO 1
LENGTH: 10
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Gaps

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Ley, Arthur Charles
Kent, Rachel Baribault
TITLE OF INVENTION: Directed Evolution of No. US20030113717Alel
Binding Proteins
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T: ROBERTS, Bruce L.
T: MARKLAND, William
T: LEY, Arthur C.
T: KENT, Rachel B.
INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.0%; Score 13; DB 10; I 100.0%; Pred. No. 8.3e+03; Itive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION: COLLINGARIA

APPLICATION NUMBER: 08/009,319

FILING DATE: CURKNOWN

APPLICATION NUMBER: 07/64,989

FILING DATE: 01-MAR-1991

APPLICATION NUMBER: 07/487,063

FILING DATE: 02-MAR-1990

APPLICATION NUMBER: 07/40,160

FILING DATE: 02-MAR-1990

APPLICATION NUMBER: 07/240,160

FILING DATE: 02-SEP-1988

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                         STATE: DC
COMDITE: USA
ZIP: 20004
COMDITER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/09/893,878
FILING DATE: 29-Jun-2001
CLASSIFICATION: <universely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: COOPET, ITAET P.
REGISTRATION NUMBER: 28005
REFERENCE/DOCKET NUMBER: LADNER 7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPHONE: 202-737-3528
                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSE: Browdy and Neimark
STREBT: 419 Seventh Street, N.W.
Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 19: US-09-893-878-19
Guterman, Sonia Kosow
Roberts, Bruce Lindsay
Markland, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-896-095-19
; Sequence 19, Application US/09896095
; Publication No. US20030219886A1
; Publication No. WSZNATION;
; APPLICANT: LADNER, Charles C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 19
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                       CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                 NUMBER OF SEQUENCES:
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Best Local Similarity
Matches 5; Conserv
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APPLICANT: Pilvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
FILE REPRENCE: P1794R1
CURRENT APPLICATION NUMBER: US 60/248,935B
CURRENT FILING DATE: 2000-11-15
PRIOR PEPLICATION NUMBER: US 60/248,985
PRIOR APPLICATION NUMBER: US 60/204,490
PRIOR APPLICATION NUMBER: US 60/204,490
PRIOR APPLICATION NUMBER: US 60/204,490
PRIOR PILING DATE: 2000-11-15
SPRIOR PILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 153
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100.0%; Pred. No. 8.3e+03;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%; Score 13; DB 9; Lv 100.0%; Pred. No. 8.3e+03; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Sequence is synthesized
                                                                                                                   NAME: COOPET, IVER P.
REGISTRATION NUMBER: 28005
REFERENCE/DOCKET NUMBER: LADNER
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                            LENGTH: 10 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECTLE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
                       FILING DATE: 02-MAR-1990
APPLICATION NUMBER: 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 26
US-09-893-878-19
US-09-893-878-19
; Sequence 19, Application US/09893878
; Publication No. US20030113717A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
     APPLICATION NUMBER: 07/487,063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: Xaa
LOCATION: 2-3, 6-9
CHER INFORMATION: Unknown amino acid
US-09-858-935B-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 67, Application US/09858935B Publication No. US20030069177A1 GENERAL INFORMATION:
                                                                                                                                                                                                               TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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Gaps

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Length 10; Indels

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Gaps
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                  50.0%; Score 13; DB 12; Length 10; 100.0%; Pred. No. 8.3e+03; cive 0; Mismatches 0; Indels
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100.0%; Pred. No. 8.3e+03;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                  US-10-098-093-18

Sequence 18, Application US/10098093

Publication No. US20030092631A1

GENERAL INFORMATION:

APPLICANT: Deshayes, Kurt D.

APPLICANT: Schaffer, Michelle L.

APPLICANT: Sidhu, Sachdev S.

TITLE OF INVENTION: IGF ANTAGONIST PEPTIDES

FILE REFERENCE: P1863R1

CURRENT APPLICATION NUMBER: US/10/098,093

CURRENT FILING DATE: 2002-03-13

PRIOR FILING DATE: 2001-03-14

NUMBER: OF SEQ ID NOS: 122

SEQ ID NO 18

LENGTH: 10

TENGTH: 10

TENGTH: 10

TENGTH: 10
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Publication No. US20030092631A1
GENERAL INFORMATION:
APPLICANT: Deshayes, Kurt D.
APPLICANT: Lowman, Henry B.
APPLICANT: Solant: APPLICANT: Sidhu, Sachdev S.
ITLE OF INVENTION: IGF ANTAGONIST PEPTIDES
FILE REPERENCE: Pla65R1
CURRENT APPLICATION NUMBER: US/10/098,093
CURRENT PILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/275,904
NUMBER OF SEQ ID NOS: 122
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
COTHER INFORMATION: Sequence is synthesized
NAME/KEY: Xaa
COTHON: 1-2, 4-7, 9-10
COTHER INFORMATION: Unknown amino acid
US-10-098-093-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Sequence is synthesized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Xaa
LOCATION: 2-3, 6-9
OTHER INFORMATION: Unknown amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 10
TYPE: PRT
ORGANISM: Artificial sequence
                  Query Match
Best Local Similarity 100.
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature

LOCATION: (1)...(2)

COTHER INFORMATION: Xaa can be any naturally occurring amino acid
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4)...(7)

OTHER INFORMATION: Xaa can be any naturally occurring amino acid
FEATURE:
NAME/KEY: misc_feature
LOCATION: (9)...(10)

OTHER INFORMATION: Xaa can be any naturally occurring amino acid
COTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-896-095-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VESULE 128

VESULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: synthetic - Class I microprotein library FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13; DB 11; Length 10;
Pred. No. 8.3e+03;
0; Mismatches 0; Indels
FILE REFERENCE: LADNER=7L

CURRENT APPLICATION NUMBER: US/09/896,095

CURRENT FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: 08/415,922

PRIOR FILING DATE: 1993-01-26

PRIOR APPLICATION NUMBER: 08/009,319

PRIOR FILING DATE: 1991-03-01

PRIOR PILING DATE: 1991-03-01

PRIOR FILING DATE: 1991-13-01

PRIOR FILING DATE: 1997-12-18

NUMBER OF SEQ ID NOS: 274

SOFTWARE: PATENTIN VETSION 3.2

SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Xaa

LOCATION: 2-3, 6-9

1 OTHER INFORMATION: Unknown amino acid

US-10-271-869-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Powatches 5; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Sequence is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 CXXXX 7
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DB 14;

50.0%; Score 13;

Query Match

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Kent, Rachel Baribault
TITLE OF INVENTION: Directed Evolution of No. US20030219722Alel
Binding Proteins
                                                                                                                                                                                                                                     Length 10;
                                                                                                                                                                                                                                50.0%; Score 13; DB 14; I
100.0%; Pred. No. 8.3e+03;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTEXT USA

ZIPTO 2004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
COMPUTER: IBM PC COMPALIDLE
COMPUTER: IBM PC COMPALIDLE
COMPUTER: IBM PC COMPALIDLE
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/009.319

FILING DATE: 1993-01-26

APPLICATION NUMBER: O7/64,989

FILING DATE: 01-MAR-1991

APPLICATION NUMBER: PCT/US89/03731

FILING DATE: 02-MAR-1990

APPLICATION NUMBER: O7/487,063

APPLICATION NUMBER: O7/487,063

FILING DATE: 02-MAR-1990

APPLICATION NUMBER: O7/240,160

FILING DATE: 02-MAR-1990

APPLICATION NUMBER: O7/240,160

FILING DATE: 02-MAR-1990

APPLICATION NUMBER: O7/240,160

ATTORNEY/AGENT INCORPATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 33
US-10-126-685-19
Sequence 19, Application US/10126685
Publication No. USZO030219722A1
GENERAL INFORMATION:
HAPPLICANT: Ladner, Robert Charles
Roberts, Bruce Lindsay
Markland, William
Ley, Arthur Charles
Ley, Arthur Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28005
REFERENCE/DOCKER NUMBER: LADNER
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPHONE: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W.
                                                                                        CTHER INFORMATION: Xaa = any amino acid
NAME/KEY: MISC_FEATURE
COCATION: (9)...(9)
CTHER INFORMATION: Xaa = any amino acid
US-10-013-815-78
                           = any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 5; Conservative
LOCATION: (2)..(5)
OTHER INFORMATION: Xaa
NAME/KEY: MISC FEATURE
LOCATION: (7)..(7)
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                                                                                                                                                                                                                                     Query Match
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                           Gaps
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                                                                                                                                                                                                                 Sequence 75, Application US/10013815
Publication No. US20030105000A1
GENERAL INFORMATION:
APPLICANT: Pero, Stephanie
APPLICANT: Pero, Stephanie
APPLICANT: Oligino, Lyn
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING GRB7
FILE REFERENCE: US/10/013/P/1048 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/013,815
CURRENT APPLICATION NUMBER: US/10/013,815
CURRENT APPLICATION NUMBER: US 60/245,755
PRIOR APPLICATION NUMBER: US 60/245,755
NUMBER OF SEQ ID NOS: 194
SOFTWARE: Patentin version 3.1
SEQ ID NO 75
LENTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 78, Application US/10013815
Publication No. US20030105000A1
GENERAL INFORMATION:
APPLICANT: Pero, Stephanie
APPLICANT: Pero, Stephanie
APPLICANT: Pero, Lyn
TILE REFERENCE: V0139/7048 (HCL/MAT)
CURRENT APPLICATION: WHERE: US/10/013, 815
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: US 60/245,755
PRIOR FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 194
SOFTWARE: Patentin version 3.1
SEQ ID NO 78
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100.0%; Pred. No. 8.3e+03;
tive 0; Mismatches 0; Indels
                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: FRT
ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: One Embodiment of General Formula
NAME/KEY: MISC_FEATURE
COTHER INFORMATION: (2)
OTHER INFORMATION: Aa = any amino acid
NAME/KEY: MISC_FEATURE
COCATION: (4)...(4)
OTHER INFORMATION: Xaa = any amino acid
NAME/KEY: MISC_FEATURE
NAME/KEY: MISC_FEATURE
NAME/KEY: MISC_FEATURE
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OTHER INFORMATION: One Embodiment of General Formula
NAME/KEY: MISC_FEATURE
100.0%; Pred. No. 8.3e+03; ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOUGATION: (6)...(9)
; OTHER INFORMATION: Xaa = any amino acid
US-10-013-815-75
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ORGANISM: Artificial Sequence
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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                                                                     1 CXXXX 5
                                                                                                            CXXXX 7
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US-10-013-815-78
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ZIP: 20004
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Best Local Similarity
Matches 5; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 CXXXX 7
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                                                                                                                                                                                                                                                                               Sequence 21, Application US/10186229
Sequence 21, Application US/10186229
Sequence 21, Application US/10186229
GENERAL INFORMATION:
APPLICANT: Dennis, Mark S.
TITLE OF INVENTION: SERUM ALBUMIN BINDING PEPTIDES FOR TUMOR TARGETING FILE REPRENCE: 11669.108US01
CURRENT APPLICATION NUMBER: US/10/186,229
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 425
SOFTWARE: Patentin version 3.1
SEQ ID NO 21
LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MISC FEATURE LOCATION: (2). (3) OTHER INFORMATION: Xaa is any naturally occurring L-amino acid PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: MISC_FEATURE LOCATION: (6)..(3)

OTHER INFORMATION: Xaa is any naturally occurring L-amino acid US-10-186-229-21
                                                                                  50.0%; Score 13; DB 15; Length 10; 100.0%; Pred. No. 8.3e+03; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 10;
                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%; Score 13; DB 15; I 100.0%; Pred. No. 8.3e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSER: Browdy and Neimark
STREET: 419 Seventh Street, N.W.
Suite 300
MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 19: US-10-126-685-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guterman, Sonia Kosow
Roberts, Bruce Lindsay
Markland, William
Ley, Arrhur Charles
Kent, Rachel Baribault
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 35
US-10-127-028-19
Sequence 19, Application US/10127028
Publication No. US20040005539A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20004
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 5, Conservative
                                                                                Query Match
Best Local Similarity 100.
Matches 5, Conservative
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 XXXXC 10
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.0%; Score 13; DB 15; Length 10; 100.0%; Pred. No. 8.3e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                      PRIOR APPLICATION TO STATE APPLICATION TO STATE APPLICATION NUMBER: US/08/009,319
FILING DATE: 1993-01-26
APPLICATION NUMBER: 07/664,989
FILING DATE: 01-MAR-1991
APPLICATION NUMBER: PCT/US89/03731
FILING DATE: 02-REP-1989
APPLICATION NUMBER: 07/487,063
FILING DATE: 02-MAR-1990
APPLICATION NUMBER: 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: COOPET, IVET P.
REGISTRATION NUMBER: 28005
REFERENCE/DOCKET NUMBER: LADNER 7
TELECOMMUNICATION:
TELEPHONE: 202-628-5197
                                                                         CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/10/127,028
FILING DATE: 22-Apr-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/126,544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W.
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ladner, Robert Charles
Guterman, Sonia Kosow
Roberts, Bruce Lindsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rachel Baribault
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Markland, William
Ley, Arthur Charles
Kent, Rachel Baribau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19, Application US/10126544 Publication No. US20040023205A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 121
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FILING DATE: 22-Apr-2002

CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:

APPLICATION DATA:

PRIOR APPLICATION NUMBER: US/08/009,319

FILING DATE: 01-XR-1989

APPLICATION NUMBER: PCT/US89/03731

FILING DATE: 01-KR-1980

APPLICATION NUMBER: 07/48,063

FILING DATE: 02-KR-1990

APPLICATION NUMBER: 07/48,063

ATTORNEY/ACENT INFORMATION:

NAME: COOPEY, Iver P.

REGISTRATION NUMBER: 08005

REGISTRATION NUMBER: 08005

REGISTRATION NUMBER: 08005

REGISTRATION NUMBER: 08005

REGISTRATION INFORMATION:

TELECHONE: 202-628-5197

TELECHONE: 202-628-5197

TELECHONE: 202-628-5197

TELECHONE: 000-19:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: procein

SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-10-126-544-19

ROUGETY MARCH

Best Local Similarity 100.0%; Pred. NO: 813e40; Indels

Best Local Similarity 00.0%; Pred. NO: 813e40; Indels

Batches S; Conservative 0; Mismatches 0; Indels
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Search completed: May 4, 2004, 06:58:52 Job time: 41 secs

3 CXXXXX 7

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

4, 2004, 06:50:57 ; Search time 52 Seconds (without alignments) 54.336 Million cell updates/sec May Run on:

US-10-046-922-33 26 1 CXXXXXXX 10 Title: Perfect score: Sequence:

Scoring table:

PAM150XX Gapop 10.0 , Gapext 0.5

1586107 seqs, 282547505 residues Searched:

28 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 10 Maximum DB seq length: 10

Post-processing: Minimum Match 50% Maximum Match 100% Listing first 100 summaries

A\_Geneseq\_29Jan04:\* 1: genesecro19R0e.\* Database :

gensequ1980s: genseqp1990s: genseqp2001s: genseqp2001s: genseqp2002s: genseqp2003ss: genseqp2003bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	ion	Carcinoem	Carcinoem	VEGFR-3 b	B lymphoc	G-CSFR bi	B Lymphoc		CX7C libr	Influenza	Degenerat	Nucleophi	Androgen	Protein t	Growth fa	Growth fa	Generic g	Synthetic	Peptide 1		Growth fa	Peptide m	Represent	Gammaherp	Insulin-1	Peptide w
	Description	Aau70627	Aau70520	Abp53930	Abj 00553	Aau79402	Abg33414	Aau98179	Ade37057	Aar88384	Aab01531	Aau85661	Aae31886	Aab73068	Abg68466	Abg68461	Aar76827	Aab31822	Aag63739	Abg68465	Abg68462	Abb57651	Abg66157	Aae19557	10	Abr41963
SUMMAKIES	ID	AAU70627	AAU70520	ABP53930	ABJ00553	AAU79402	ABG33414	AAU98179	ADE37057	AAR88384	AAB01531	AAU85661	AAE31886	AAB73068	ABG68466	ABG68461	AAR76827	AAB31822	AAG63739	ABG68465	ABG68462	ABB57651	ABG66157	AAE19557	ABJ15256	ABR41963
	DB	2	'n	Ŋ	Ŋ	'n	'n	ហ	7	N	m	'n	9	4	Ŋ	Ŋ	N	4	4	ហ	Ŋ	ល	Ŋ	'n	Ŋ	w
	Length	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
dł	Query Match	100.0	100.0	100.0	100.0	0	100:0	8	61.5	~	57.7	7.	۲.	'n	m.	m,	ö	ö	50.0	ó	ö	o.	٥.	20.0	ö	20.0
	Score						26					15		14	14	14	13	13	13	13	13	13	13	13	13	13
	Result No.		N)	e	4	w	ø	7	ω	თ	10	11	12	13	14	15	16	17	18			21				25

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Gaps

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Query Match
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 10; Conservative 0; Mismatches 0; Indels

Sequence 10 AA;

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Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypoteneive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypotteneion; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
VEGFR-3 binding peptide SEQ ID NO:33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LICW) LICENTIA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JAN-2002; 2002WO-IB000099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7-JAN-2001; 2001US-0262476P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Koivunen E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-691521/74.
                                                                                                                                                                                                                                                                                                                                                             Misc-difference 8
                                                                                                                                                                          Key
Misc-difference
                                                                                                                                                                                                                 Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200257299-A2
                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JUL-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alitalo K,
                                                                                                                                             Synthetic
 The invention relates to a polypeptide having the ability to bind carcinoembryonic antigen (CEA, an immunoreactive glycoprotein) which is overexpressed in adenocarcinomas of endodermally derived digestive system epithelia and foetal colon. The peptides do not react with non-specific cross-reacting antigen NCA. The peptides, labeled with a radioactive compound, such as indicative of CEA-associated disease and may be subject, which is indicative of CEA-associated disease and may be conjugated with a therapeutic agent such as radioactive or chemotherapeutic agent, toxin or enzyme is useful for treating a CEA associated disease such as colon, lung, breast, cervical, ovarian, stomach, bladder, pancreatic or oesophageal cancer in a subject. The peptides are useful for imaging, localising and targeting tumours exhibiting CEA by radioimaging, magnetic resonance imaging or X-ray imaging. Phage products displaying the peptides are also useful for detection and diagnosis of cancer associated with the expression of CEA in cells and tissues. The present sequence is a representative peptide, or an example of a library, of the CEA binding peptides of the invention
                                                                                                                                        Carcinoembryonic antigen; CEA; non-specific cross-reacting antigen; NCA; adenocarcinoma; cancer; tumour; immunoreactive glycoprotein; indium; technetium; cytostatic; phage display.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel carcinoembryonic antigen binding peptides for detecting, imaging, localizing and targeting tumors exhibiting the antigen, especially for treating colon cancer in humans and animals.
                                                                                                                Carcinoembryonic antigen representative binding peptide #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 26; DB 5; Length 10; 100.0%; Pred. No. 1.3; o; Indels iive 0; Mismatches 0; Indels
                           AAU70520 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 46; 119pp; English.
                                                                                                                                                                                                                                                                                      03-APR-2001; 2001WO-US010689.
                                                                                                                                                                                                                                                                                                                     03-APR-2000; 2000US-00541345.
                                                                                    14-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100
                                                                                                                                                                                                                                                                                                                                                                            Ladner RC;
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-049088/06.
                                                                                                                                                                                                                                                                                                                                               (DYAX-) DYAX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10 AA;
                                                                                                                                                                                                                                WO200174849-A2.
                                                                                                                                                                                                                                                            11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                            Rondon IJ,
                                                                                                                                                                                                   Synthetic
                                                       AAU70520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
RESULT 2
               AAU70520
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/note= "X is tryptophan or a conservative substitution"

/note= "X is glycine or a conservative substitution"

Kubo H;

note= "X is isoleucine or a conservative substitution" 'note= "X is threonine or a conservative substitution"

note= "X is tryptophan or a conservative substitution"

/note= "X is leucine or a conservative substitution"

'note= "X is tyrosine or a conservative substitution"

'note= "X is glycine or a conservative substitution"

Location/Qualifiers

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                                                                                                                                                                                                                              The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive, antidabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, there is spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, heamangioms and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 100.0%; Score 26; DB 5; Length 10; Similarity 100.0%; Pred. No. 1.3; 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                   Claim 3; Page 78; 149pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CXXXXXXXX 10
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Matches
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ABP53930 standard; peptide; 10 AA.

1 CXXXXXXXC 10 CXXXXXXXC 10

ò a (first entry)

09-JAN-2003

ABP53930;

ABP53930 ID ABP5 XX AC ABP5 XX DT 09-J

RESULT 3

hypergammaglobulinaemia, blood clotting disorders, ischaemia, and neurodegenerative diseases. The present sequence is a B lymphocyte stimulator protein binding peptide

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The present invention relates to the treatment, prevention or ameliotration of a disease or disorder associated with: aberrant B lymphocyte stimulator (BLyS), BLyS receptor expression or activity; cells of haematopoietic origin; or proliferative disease; and reducing, thinbitting or stimulating immunoglobulin production, Beal proliferation and graft rejection involving administration of BLyS binding polypeptides are used in the treatment, prevention or mealloration of diseases such as immune system diseases, proliferative diseases, diseases of cells of hematopoietic origin, graft rejection; allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label≈ Ala, Asn, Arg, Gln, Leu, Met, Ser, Trp, Tyr, Val
                                                                                                                                                                                                                                                                             immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
neuroprotective; cytostatic; immunostimulant; antitumcur; anti-HIV;
antiathmatic; antiallergic; thyromimetic; antianaemic; haemostatic;
dermatological; antiinflammatcry; cardiant; ophthalmological; uropathic;
antidiabetic; antithyroid; antidepressant; hepatotropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The treatment of various diseases e.g. rheumatoid arthritis, comprises administering B Lymphocyte stimulator binding polypeptide.
                                                                                                                                                                                                                  B lymphocyte stimulator protein binding protein; BLyS; immune disease; allergy; profilerative disease; infectious disease; arteriosclerosis; inflammatory disorder; hypergammaglobulinaemia; blood clotting; inchammatory disease; soluting; inchaemia; graft-versus-host disease; neurodegenerative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gln, His, Ile, Leu, Lys, Met, Phe,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Ala, Arg, Asn, Gly, His, Lys, Ser, Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phe,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phe, Pro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thr
                                                                                                                                                                                     B lymphocyte stimulator protein binding peptide #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Met,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                label= Ala, Arg, Asp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                label= Ala, Arg, Asn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fleming TL,
                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 69; Page 234; 387pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ile,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 His,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leu,
                                                                                            ABJ00553 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-AUG-2001; 2001WO-US025850.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-AUG-2000; 2000US-0226700P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Asp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= His,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= Asp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              label= Ile,
                                                                                                                                                         (first entry)
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                  10
CXXXXXXXC
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                                                                                                                                                                                                                                                                                                                                                                           Unidentified
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                                                                                                                                                        05-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                    glu,
                                                                                                                                                                                                                                                                                                                                                             Val,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Thr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leu,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Val,
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       Ser,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Leu,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ser,
                                                                                                                                                                                                                                                    G-CSFR; granulocyte-colony stimulating factor receptor; cytokine; haematopoietic growth factor; neutrophil proliferation; AIDS; neutrophil differentiation, acquired immunodefictency syndrome; chemotherapy-induced neutropaenia; community acquired pneumonia; depressed neutrophil count; immunostimulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tyr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Met,
                                                                                                                                                                                                                                                                                                                                                                                                       Ala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Asp,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Ser,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ile,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leu,
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                                                                                                                                                                                                                                                                                                                                                                                                       Val,
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                                                                                                                                                                                                                                                                                                                                                               Leu,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Asn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thr,
                                                         Length 10,
                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                             Gly,
                                                                                                                                                                                                                                                                                                                                                                                                       Ile,
                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Glu, Val, Trp, Phe, Met, Ala,
Tyr, Gly, Pro
/note= "Especially Glu or Trp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Val, Ile, Gly, Gln, Trp, Met, Asp, Cys, Glu, Ala
/note= "Especially Val, Ile or Tyr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Asn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tyr, Val, Asn, Leu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trp, Tyr, Val, Phe,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= His, Ala, Trp, Tyr, Val, Pho
Ser, Asp, Pro, Gly
/note= "Especially Trp, Tyr or Phe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lly, Gln, Cys, Thr
note= "Especially Met, Tyr or Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tyr, Arg, Ile, Lys, T
e, Asp, Pro, Gly, Gln
sially Cys or Met"
                                                                                                                                                                                                                                                                                                                                                                                                    /label= Met, Gly, Arg, His, Asp, 1
Asn, Phe, Tyr, Pro, Cys, Trp, Thr
/note= "Especially Asp or Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |Jabel= Met, Glu, Trp, Leu, Pro, P
Tyr, Gln, Ser, Arg, Gly, His, Asp
|note= "Especially Met or Leu"
                                                                              ö
                                                                                                                                                                                                                                                                                                                                                             /label= Ala, Asn, Ser, Phe, Asp,
Pro, Gln, His, Met, Lys
/note= "Especially Asp or Pro"
                                                           Š,
                                                                  red. No. 1.3;
Mismatches
                                                          100.0%; Score 26; DB 100.0%; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Cys, Tyr, Arg,
Ala, Thr, Phe, Asp, Pro
/note= "Especially Cys
                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label= Met, Phe, T
                                                                                                                                                                                                                                      G-CSFR binding generic peptide #1.
                                                                                                                                                                         AAU79402 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= His,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUL-2001; 2001WO-US023046
                                                                                                                                                                                                                  (first entry)
                                                                    Local Similarity 100.
ses 10; Conservative
                                                                                                   10
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                                                                                                                      1 CXXXXXXXX
                                                                                                  1 CXXXXXXXC
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                                       Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                              AAU79402;
                                                           Query Match
                                                                      Best Loc
Matches
                                                                                                                                                    RESULT 5
AAU79402
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                                                                                                    à
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synovial fluid; saliva; mucus.

WO200216412-A2

Mceowen-Merrill B;

Piplani S,

Duffin DJ,

Balu P,

Synthetic

28-FEB-2002

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Novel compounds, useful for treating depressed neutrophil count, comprise peptide chains of approximately 6 to 40 amino acids in length that bind to granulocyte-colony stimulating factor receptor.
                                          Claim 1; Page 51; 90pp; English.
20-JUL-2000; 2000US-00620091
      (GLAX ) GLAXO GROUP LTD
                      WPI; 2002-329382/36.
             SE,
PJ;
                Schatz
             wirla
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ô Gaps ; 0 100.0%; Score 26; DB 5; Length 10; 100.0%; Pred. No. 1.3; ive 0; Mismatches 0; Indels Query Match Best Local Similarity 100. Marches 10; Conservative CXXXXXXX 10 Sequence 10 AA; à

CXXXXXXXX 10 g

B Lymphocyte Stimulator (BLyS) binding peptide #9. ABG33414 standard; peptide; 10 AA. (first entry) 15-JUL-2002 ABG33414; RESULT 6 8222528282 82225282828

B Lymphocyte Stimulator protein; B Lymphocyte Stimulator binding peptide; BLyS; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;

Trp, Val, Ile /note= "When Xaa at position 2 is Val, Xaa at position 3 is Phe and Xaa at position 7 is Tyr, Xaa at this position label= Thr, Ser, Asp, Tyr, Ala, Phe, Pro, Leu, Gly, His,

/label= Phe, Ile, Trp, Pro

Misc-difference 4

Location/Qualifiers

label= Val, Ile

Misc-difference 2

Synthetic.

Misc-difference

Prostate specific antigen; PSA; binding agent; peptidomimetic; prostatic disease; cytotoxic agent; gene therapy vector; imaging agent; activation step; cytostatic.

Prostate specific antigen (PSA) formula I peptide.

(first entry)

12-AUG-2002

AAU98179 standard; peptide; 10 AA.

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                                                                                                                                                                                                                                                               New B-lymphocyte stimulator binding polypeptide useful in detecting or isolating BLyS or BLyS-like polypeptide comprises a specified amino acid
                                                                                                                                                                                                                                                                                                                                                   The invention relates to a B Lymphocyte Stimulator (BLyS) binding polypeptide. BLyS binding peptides bind BLyS or BLyS-like proteins reversibly or irreversibly. The binding peptides are used in detection, isolation and/or purification of BLyS in a solution such as water or a buffer solution, as well as any fluid and/or cell obtained from an individual biological fluid, body tissue, body cell, cell line, tissue culture or other source containing BLyS or BLyS-like polypeptides. Diological fluids include sera, plasma, lymph, blood, blood fraction, urine, synovial fluid, spinal fluid, saliva and mucous. Sequences ABG33406-33415, ABG3423-3555, ABG33588-33846, ABG33848-33850 and ABG33852-33862 represent BLyS binding peptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
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                                                                                                                                                                                                                                                                                                                                Claim 9; Page 99; 269pp; English.
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0
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Best Local Similarity 100.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CXXXXXXX 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10 AA;
                                                                                                                                                                                                                                                                                                      sequence,
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Ladner RC;

Fleming TJ,

Seltzer JP, Potter MD,

(DYAX-) DYAX CORP.

WPI; 2002-351647/38.

17-AUG-2001; 2001WO-US025891. 18-AUG-2000; 2000US-0226489P

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Binding agents for prostate-specific antigen useful e.g. for treatment or
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frp, val, lie for the form of 
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firp, Val, Val, Aa at position 3

firp, AB, Tyr, Ala, Phe, Pro, Ieu.

And Exa at position 2 is Val, Xaa at position 3 is Ile

and Xaa at position 7 is Asn, Xaa at this position is

preferably Tyr, Asp, Gly, His, Tyr, Pro, Val, When Xaa at

position 7 is Ile, Xaa at position 3 is Phe and Xaa at

position 7 is Tyr or Asp, Xaa at this position is

preferably Glu, Pro, Asp, Ser, Tyr, Gly, Phe, Ile, Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trp, Val, ile
//note= "When Xaa at position 2 is Val, Xaa at position 3
is Phe and Xaa at position 7 is Tyr, Xaa at this position
is preferably Thr, Ser, Asp, Tyr, Ala, Phe, Pro, Leu.
When Xaa at position 2 is Val, Xaa at position 3 is Ile
and Xaa at position 7 is Asn, Xaa at this position is
preferably Tyr, Asp, Gly, His, Tyr, Pro, Val, When Xaa at
position 2 is Ile, Xaa at position 3 is Phe and Xaa at
position 7 is Tyr or Asn, Xaa at this position is
preferably Glu, Pro, Asp, Ser, Tyr, Gly, Phe, Ile, Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jeabel= Thr, Ser, Asp, Tyr, Ala, Phe, Pro, Leu, Gly, His, Trp, Val, 11e

/note= "When Xaa at position 2 is Val, Xaa at position 3 is Phe and Xaa at position 7 is Tyr, Xaa at this position is preferably Thr. Ser, Asp, Tyr, Ala, Phe, Pro, Leu. When Xaa at position 2 is Val, Xaa at position 1 is Asp, Tyr, Ala, Phe, Pro, Ieu. When Xaa at position 2 is Na, Xaa at this position is preferably Tyr, Asp, Gly, His, Tyr, Pro, Val, When Xaa at position 2 is Ile, Xaa at position 3 is Phe and Xaa at position 7 is Tyr or Asp, Xaa at this position is position 7 is Tyr or Asp, Xaa at this position is preferably Glu, Pro, Asp, Ser, Tyr, Gly, Phe, Ile, Leu"
is preferably Thr, Ser, Asp, Tyr, Ala, Phe, Pro, Leu.
When Xaa at position 2 is Val, Xaa at position 3 is Ile
and Xaa at position 7 is Asn, Xaa at this position is
preferably Tyr, Asp, Gly, His, Tyr, Pro Val. When Xaa at
position 2 is Ile, Xaa at position 3 is Phe and Xaa at
position 7 is Tyr or Asn, Xaa at this position is
preferably Glu, Pro, Asp, Ser, Tyr, Gly, Phe, Ile, Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               label = Thr, Ser, Asp, Tyr, Ala, Phe, Pro, Leu, Gly, His,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ser, Asp, Tyr, Ala, Phe, Pro, Leu, Gly, His,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leinonen J, Naervaenen A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Tyr, Asn, Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               label= Thr, S
rrp, Val, Ile
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                                                                                            The present invention relates to a new binding agent selective for free prostate-specific antigen (PSA). The invention comprises a peptide at least 6 amino acids long including at least one pair of Cysteine residues separated by at least 2 amino acids and cyclised through a disultide bond or a peptidomimetic having a spatial conformation similar to the peptide. The binding agents of the invention are useful for treating and diagnosing diseases associated with PSA-producing cells, especially benign and malignant prostatic disease. The invention can also be used to isolate and purify various molecular forms of PSA and for targeted delivery of cytocoxic agents, gene therapy vectors and imaging agents of the invention have a binding apecificity that can not be obtained with antibodies. The present amino acid sequence represents the prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interfacial biomaterial; binding agent; biological substrate; cytostatic;
Tie2 receptor antagonist; cell culture; biological array;
transplant cell; transplant tissue; Tie2 receptor modulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New interfacial biomaterial having binding agents that binds a non-biological and biological substrate, useful in cell culture, in the preparation of biological arrays, and for diagnostic and therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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diagnosis of benign and malignant prostatic disease are peptides peptideminetics.
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                                                                                                                                                                                                                                                                                                                                                                                                       ch 100.0%; Score 26; DB 5; Length 10; 1 Similarity 100.0%; Pred. No. 1,3; 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                      specific antigen formula I peptide of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADE37057 standard; peptide; 10 AA.
                                                                 Claim 4; Page 64; 105pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CXXXXXXXX 10
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Best Local S:
Matches 10,
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ADE37057
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interface between the target non-biological substrate and the target biological substrate, or a non-binding domain substantially lacks binding to a target biological substrate. (I) has cytostatic activity, and can be used as a Tie2 receptor antagonist. The methods and compositions of the present invention can be used in cell culture of fibroblasts, endothelial cells, seme cells, embryonic and newborn tissue cells and osteoblasts, in the preparation of biological arrays, in the enhancement of an interaction between biological materials, for coating implants for in vivo use, for coating donor transplant cells or tissues, for diagnostic and therapeutic interface, and for modulating Tie2 receptors in tumour angiogenesis. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying cpds. that inhibit palmitylation of influenza haemagglutinin - and thus prodn. of influenza virus, potentially useful for treating influenza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "0-40 amino acids of haemagglutinin transmembrane region upstream of the depicted sequence"
                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemagglutinin; palmitate; influenza; cytoplasmic domain; treatment; palmitylation; inhibitor; viral assembly.
                                                                                                                                                                                                                                         61.5%; Score 16; DB 7; Length 10; 100.0%; Pred. No. 1.5e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label= Lys, Ile, Met, Cys, Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           label= Arg, Asn, Gln, Thr, Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Ile, Phe, Tyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        AAR88384 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Influenza palmitylation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               label= Ser, Asn
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                        2 CXXXXXXX 9
                                                                                                                                                                                present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Influenza virus.
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                                                                                                                                                                                                                 Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR88384;
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amino acids of the transmembrane region upstream of the depicted sequence, of influenza haemagajutinin (HA). The peptide may be used to compete with viral HA as the substrate of palmitylation, and therefore may be useful as an influenza HA palmitylation inhibitor. Such an inhibitor will inherefere with viral assembly, but not with palmitete biosynthesis (which is important for cellular metabolism and energy prodn.) and is therefore a potentially useful influenza treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymer; blomaterial; conjugate; hydrogel; drug delivery; adhesive; sealant; tissue engineering; wound healing; scaffold; cell transplant; adhesion prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing polymeric biomaterials by polymerizing two or more precursor
                                       opt. with 0-40
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                            .0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note⇒ "Any amino acid other than cysteine"
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                                                                                                                                                                                                          Match S7.7%; Score 15; DB 2; Length 10; Local Similarity 100.0%; Pred. No. 3.1e+03; les 7; Conservative 0; Mismatches 0; Indels
                                    The present peptide is based on the cytoplasmic domain, amino acids of the transmembrane region upstream of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lutolf M, Pratt A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
            Disclosure, Page 26; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       AAB01531 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Degenerate telechelic peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Tirelli N, Vernon B;
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                                                                                                                                                                                                                                                                             4 XXXXXXC 10
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                                                                                                                                                                                    Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                      AAB01531;
                                                                                                                                                                                                                   Query Match
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components (e.g. polymer, protein or peptide) of the biomaterial, useful for delivering therapeutic molecules to a subject and as adhesives or
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Disclosure; Page 29; 119pp; English.

combining two or more precursor components (e.g. polymer, protein or the biomarerial under conditions that allow polymerization of the biomarerial under conditions that allow polymerization of between a components. Polymerization occurs through self selective reaction between a strong nucleophile and a conjugated unsaturated bond or a hydrogels can be used in a variety of applications. They can be used to deliver therapeutic molecules to a subject, as adhesives or sealants (e.g. sealing air leaks on the lung), as tissue engineering and wound healing scaffolds, and as cell transplant devices. The biomaterials are post-traumatic adhesions A method of making polymeric biomaterials is described comprising

###X#X00000000000XX

Sequence 10 AA;

0; Gaps 57.7%; Score 15; DB 3; Length 10; 100.0%; Pred. No. 3.1e+03; ive 0; Mismatches 0; Indels Local Similarity 100. 1 CXXXXXX 7 Query Match Matches

CXXXXXX B

AAU85661 standard; peptide; 10 AA. AAU85661;

21-MAY-2002

Nucleophile containing peptide consensus sequence #1.

(first entry)

infection; adhesion; thrombosis; restenosis; adhesive; sealant; tissue engineering; wound healing scaffold; cell transplant device. Biomaterial; vasotropic; anticoagulant; thrombolytic; vulnerary;

Synthetic.

WO200192584-A1.

06-DEC-2001.

04-JUN-2001; 2001WO-US018101

02-JUN-2000; 2000US-00586937.

(BIDG-) EIDGENOESSISCHE TECH HOCHSCHULE ZUERICH. UNIV ZURICH. (UYZU-)

Schoenmakers R; Hubbel JA, Elbert D,

WPI; 2002-205802/26.

New biomaterial useful for medical treatment comprises an active or a binding group and has an ester or amide bond onto the active or binding

Disclosure; Page 66; 222pp; English.

The invention relates to a biomaterial comprising an active or a binding group and has an ester or amide bond onto the active or binding group. Also included is a biomaterial (II) formed from the cross-linking of at least uncluded is a components of formula D-Y-C(0) -(CH 2) n-S-(CH 2) cox-P', D-Y-C(0) -(CH 2) n-NH-(CH 2) 2-COX-P', D-Y-C(0) -(CH 2) n-NH-(CH 2) 2-COX-P', D-Y-C(0) -(CH 2) n-NH-(CH 2) n AAUUS 11)
AAUUS AA

conjugate addition reaction to form a precursor component and (a) crosslinking the uncoupled conjugated unsaturated groups in at least one
precursor component. D = active or binding group; Y = 0, NH or N; L =
linear or branched linker; X = 0 or N; P' = water-soluble or water swellable polymer containing conjugated unsaturated groups; U = product
of the addition of a nucleophile to an electrophile that is attached to
the water-soluble or water-swellable polymer; and n = 2 - 3. The
longaterials are useful for treating or preventing disease, disorder or
infection in a mammal e.g. human, for preventing adhesions, thrombosis or
cestenosis in a mammal and for delivering the active compound (preferably
protein or peptide) to a cell, tissue, organ, organ system or a body of a
mammal as adhesives or scalants, as tissue engineering and wound healing
scaffolds and as cell transplant devices. The bond of the biomaterial has
a half life of 1 hour - 1 year (preferably 1 ady - 9 months, especially 2
days - 2 months) in an aqueous solution at pH 7.4 and 37plusoC. Thus the
biomaterial releases the therapeutic compound over a clinically relevant time-frame. The present sequence is a consensus sequence for a peptide containing reactive thiol (cysteines) groups suitable for inclusion in Gaps ; 57.7%; Score 15; DB 5; Length 10; 100.0%; Pred. No. 3.1e+03; ive 0; Mismatches 0; Indels the biomaterial of the invention Query Match Best Local Similarity 100.0 Matches 7; Conservative 1 CXXXXXX 7 2 CXXXXXX 8 Sequence 10 AA; ઠે

RESULT 12 AAE31886

AAE31886 standard; peptide; 10 AA.

AAE31886;

07-MAR-2003 (first entry)

Androgen receptor binding peptide #137.

Androgen receptor, androgen-associated disorder, prostate cancer, acne, benign prostatic hypertrophy, hirautism, androgen insensitivity syndrome, andle pattern baldness, Stein-Leventhal syndrome; infertility, cytostatic; X-linked spinal bulbar muscular atrophy, antiseborrheic; dermatological; depilatory; androgen receptor binding peptide. 

Unidentified

/note≈ "Linked to Xa-Y1; Where Xa is independently a direct bond or a peptidic structure comprising from about 1-25 amino acid residues and Y1 is hydrogen, alkyl or acyl" Location/Qualifiers Misc-difference

'note≈ "Xaa is an aromatic amino acid or Thr" Misc-difference 3 Misc-difference

/label= Gly, Phe, Gln, Arg, Met, Trp /label= Asp, Glu Misc-difference

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The present invention provides novel trifluoromethyl sulfonyl and trifluoromethyl sulfonamido compounds which modulate the activity of protein phosphateses are involved in signal transduction, and the compounds can be used to treat diseases mediated by protein phosphatase action, including cancer, immune discorders such as anamala and immunodeficiency, diabetes, rheumatoid arthritis, and as neurodegenerative diseases, infections and osteoporosis. The present sequence comprises a consensus sequence of the protein phosphatase active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Growth factor receptor-bound protein 7; Grb7; ligand; antagonist; cytostatic; cancer; phage display; tumour; metastasis; breast cancer; oesophageal cancer; kidney disorder; liver disorder; gonad disorder; breast disorder; cosophageal disorder; pancreatic disorder; proseste disorder; small intestine disorder; placental disorder; colon disorder; lung disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             New arcmatic and heterocyclic compounds containing trifluoromethylsulfonyl groups, used to treat cancers, diabetes, neurological degenerative diseases and osteoporosis, are protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Growth factor receptor-bound protein 7 antagonist example #20.
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Pred. No. 6.3e+03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                  Liang C, Ramphal J,
3, Koenig M;
                                                           2. .9
/label= Xaa
/note= "Xaa=unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Page 15, 262pp, English
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.8%; Scur.
100.0%; Pre
                                                                                                                             /label= Ser, Thr
                                   label= Ile, Val
                                                                                                                                                                                                                                                                                                                                                                       Tang PC, Li
Mcmahon G,
                                                                                                                                                                                                                                        25-AUG-2000; 2000WO-US023293.
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Li S, Mattson MN,
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Best Local Similarity
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   Key
Misc-difference
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                                                       Misc-difference
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New peptide modulators of androgen receptor, useful for treating androgen -associated disorder, e.g. prostate cancer, particularly hormonally refractive prostate cancer, colon cancer, lung cancer, acne, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to novel peptide modulators of androgen receptor. The peptides of the invention are useful for treating androgen-associated disorders such as prostate cancer, particularly hormonally refractive prostate cancer, colon cancer, lung cancer, benign prostatic hypertrophy, acne, hirsutism, male pattern baldness, Stein-Leventhal syndrome, androgen insensitivity syndrome, infertility, endometrial cancer and X-linked spinal bulbar muscular atrophy. The present sequence
                                                                                                                                                                     Incre= "Linked to Xb-Y2; Where Xb is independently a direct bond or a peptidic structure comprising from about 1-25 amino acid residues and Y2 is -04, amino or monosubstituted or disubstituted amino"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein phosphatase; signal transduction; trifluoromethyl sulfonyl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 trifluoromethyl sulfonamido, diabetes, immune disorder; infection; rheumatoid arthritis; neurodegenerative disease; cancer; infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                     label= His, Asp, Ser, Ala, Leu, Met, Trp
                                                                                                 'label= Pro, Trp, Thr, Leu, Phe, Tyr, Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15; DB 6; I Pred. No. 3.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Findeis MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is an androgen receptor binding peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB73068 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 67; Page 41; 68pp; English.
                         label= Asp, Glu
                                                               'label= Tyr, Trp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.7%;
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28-JAN-2002; 2002US-0352399P.
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Best Local Similarity 90.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (PRAE-) PRAECIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CXXXXXXXC 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Joyal JL, Mueller J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-067363/06.
         Misc-difference
                                             Misc-difference
                                                                                 Misc-difference
                                                                                                                     Misc-difference
                                                                                                                                                           Misc-difference
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                                                                                                                                                                                                                                                                                                          19-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hirsutism
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osteoporosis, are protein tyrosine

Blitz J;

Jallal B,

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Gaps

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WO200236142-A2

Unidentified

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Oligino L;

Pero SC,

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The invention relates to treatment or prophylaxis (W1) of a subject having a disorder characterised by abnormal interaction of Grb7 (Growth Eartor receptor-bound protein 7 and a Grb7 ligand, comprising a daministering to a subject in need of the treatment, a non-phosphorylated administering to a subject in need of the treatment, a non-phosphorylated peptide comprising a sequence (S1, Tyr-Ala-Asn, Tyr-Glu-Asn and Tyr-Asp-Csc peptide comprising a sequence (S1, Tyr-Ala-Asn, Tyr-Glu-Asn and Tyr-Asp-Csc of its functional equivalent, in an amount effective to inhibit the disorder. Also included are peptide antagonists/inhibitors of Grb7, uncleic acids encoding the antagonists, an expression vector comprising crb and a most cell transformed or transfected with the vector, screening (M2) a molecular library to identify a compound that inhibits interaction between Grb7 and a peptide antagonist and a phage display library comprising Grb7 and a peptide antagonist or prophylaxis or treatment of a subject having a disorder characterised by abnormal concernation of Grb7 and a Grb7 ligand, including breast or oesophageal cancer, primary tumour or metastasis, or disorders in kidney, liver, gonads, breast, oesophagus, pancreas, prostate, small intestine, concernation, ovary, testes and lung. The present sequence is a generic example of a Grb7 peptide antagonist of the invention
                                                                                                                                                                                                                                                                       Treatment or prophylaxis of a subject having a disorder characterized by abnormal interaction of \operatorname{Grb7} and a \operatorname{Grb7} ligand, involves administering to a non-phosphorylated peptide to a subject in need of the treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic, cancer, phage display, tumour, metastasis, breast cancer, oesophageal cancer, kidney disorder, liver disorder, gonad disorder, breast disorder, oesophageal disorder, pancreatic disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prostate disorder, small intestine disorder, placental disorder, colon disorder, ovary disorder, testicular disorder, lung disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Growth factor receptor-bound protein 7; Grb7; ligand; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Growth factor receptor-bound protein 7 antagonist example #15.
                                                                                                                                               UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 120; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG68461 standard; peptide; 10 AA.
                                                              05-NOV-2001; 2001WO-US047400.
                                                                                                       03-NOV-2000; 2000US-0245755P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
es 6; Conservative
                                                                                                                                                                                                                                    WPI; 2002-547451/58
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The invention relates to treatment or prophylaxis (M1) of a subject having a disorder characterised by abnormal interaction of Grb7 (Growth factor receptor-bound protein 7 and a Grb7 ligand, comprising to a subject in need of the treatment, a non-phosphorylated administering to a subject in need of the treatment, a non-phosphorylated comprising a sequence (S1, Tyr-Ala-Asn, Tyr-Glu-Asn and Tyr-Asp-peptide comprising a sequence (S1, Tyr-Ala-Asn, Tyr-Glu-Asn and Tyr-Asp-comprising a sequence (S1, Tyr-Ala-Asn, Tyr-Glu-Asn and Tyr-Asp-comprising or the functional equivalent, in an amount effective to inhibit the compound that inhibits or nucleic acids encoding the antagonists, an expression vector comprising the nucleic acids encoding the antagonists, an expression vector comprising the nucleic acid, a host cell transformed or transfected with the vector, comprising confinence of the nucleic acid, a host cell transformed or transfected with the vector, interaction between Grb7 and a peptide antagonist and a phage display interaction of Grb7 and a Grb7 ligand, including breast or oesophageal cancer, primary tumour or metastasis, or disorders in kidney, liver, concert, primary tumour or metastasis, or disorders in kidney, liver, concert, primary tumour or metastasis, or disorders in kidney, liver, concert, primary tumour or metastasis, or disorders in kidney, liver, concert, primary colon, ovary, cestes and lung. The present sequence is a generic example of a Grb7 peptide antagonist of the invention
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                                                                                                                                                               Treatment or prophylaxis of a subject having a disorder characterized by abnormal interaction of Grb7 and a Grb7 ligand, involves administering to a non-phosphorylated peptide to a subject in need of the treatment.
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Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 6; Conservative 0; Mismatches 0;
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                                                     (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE
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                                                                                                                                                                                                                                                      Disclosure; Page 118; 186pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR76827 standard; peptide; 10 AA.
                                                                                             Oligino L;
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                03-NOV-2000; 2000US-0245755P.
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                                                                                                                                   WPI; 2002-547451/58.
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                                                                                             Pero SC,
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                                                                                             Krag DN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 16
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Gaps

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Length 10; 0; Indels

Score 14; DB 5; Le Pred. No. 6.3e+03; 0; Mismatches 0;

53.8%; SCUL-100.0%; Pre

CXXXXX 6 CXXXXX 6 placental disorder;

(first entry)

05-NOV-2001; 2001WO-US047400.

WO200236142-A2

10-MAY-2002

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AAR76827 defines a class of generic TSAR (Totally Synthetic Affinity Reagent) library peptides, which bind specifically to glutathione-Stransferase (GST) is a dimeric enzyme that conjugates glutathione to various other substrates, including products of tissue damage and carcinogens. Its role in the cell seems to be in detoxification. The TSAR are new and/or improved heterofunctional binding fusion proteins that have affinity for the ligand vinculin, and can be used to modulate the activity of the ligand (or its binding proteins), e.g. in bindedicine, cacalysis, pharmaceuticals, etc. Other TGARs can be designed to bind dynein and glutathione-transferase. Typical applications are: (i) inhibition of GST to treat cancers that produce high levels of this enzyme; (ii) altering mobility/attachment of malignant cells, modulating platelet release and blood clotting, for TSARs directed against vinculin; (iii) TSARs against dynein are used to modulate nerve cell activity, sperm motility, mobility of protozoa, etc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fibrin, fibrin-binding peptide, deep-vein thrombosis, pulmonary embolism, cardiogenic thrombosis, atherosclerosis; myocardial infarction; lupus; reperfusion ischemia; stroke, peritoneal adhesion; rheumatoid arthritis; septic arthritis, thrombotic thrombosytopenic purpuas, hypoxia; tumour; diabetic retinopathy; autoimmune disorder, inflammatory disorder.
                                                                                                                                                                                                                                                                                Identifying peptide(s) that bind specifically to dynain, vinculin or enzymes, eg. glutathione-S-transferase - by screening random peptide libraries, useful e.g. in immunoassays, affinity purification., tumour treatment, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%; Score 13; DB 2; Length 10; 100.0%; Pred. No. 1.3e+04; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic peptide which is able to bind fibrin.
 /label= Asp, Ser, Gly, Met
                                                                                                                                                                                                                                                                                                                                                                           Claim 28; Page 86-87; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB31822 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label= Asn, Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Gly, Tyr
                                                                                                        95WO-US001286.
                                                                                                                                         94US-00189331.
                                                                                                                                                                                                                  Sparks AB
                                                                                                                                                                          (UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
....hes 5; Conservative
                                                                                                                                                                                                                                                 WPI; 1995-275411/36.
                                                                                                                                                                                                                Adey NB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXXXX 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10 AA;
                                                                                                        31-JAN-1995;
                                                                                                                                       31-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAY-2001
                                  WO9520601-A1
                                                                       03-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                               Кау ВК,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1'
AAB31822
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The present sequence represents a synthetic peptide which binds to fibrin. Fibrin-binding peptides of the invention are useful for the detection and treatment of deep-vein thrombosis, plumonary embolism, cardiogenic thrombosis, atheroscalerosis, myocardial infarction, reperfusion ischemia, stroke, peritoneal adhesions, rheumatoid arthritis, tumous, diabetic arthritis, thrombocic thrombocytopenic purpura, hypoxia, tumours, diabetic retinopathy, autoimmune and inflammatory disorders; and for imaging by e.g. MRI (magnetic resonance imaging), ultrasound, optical, sonoluminescence, photoacoustic or nuclear imaging techniques, and localizing fibrin containing thrombi or other fibrin specific pathophysiologies. They are also useful for the detection, isolation or purification of fibrin in or from a solution containing it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insulin-like growth factor; IGF, IGF-1; IGF binding protein; IGFBP; hyperglycemic disorder; obesity-related disorder; neurological disorder; cardiac disorder; anabolic disorder; renal disorder; neuroprotection; immunological disorder; kidney regeneration; degenerative disorder; hypoxia, wound healing; cardiac regeneration; degenerative disorder; metabolic stress; growth hormone deficiency; diabetes; short stature; osteoporosis; obesity.
                                                                                                                                                                                                                                                                                                                                                                              New fibrin-binding polypeptides useful for detection and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.0%; Score 13; DB 4; Length 10; 100.0%; Pred. No. 1.3e+04; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide library for identification of IGF-1 agonists.
                                                                                                                                                                                                                                                                                                           Wescott CR, Nair SA, Kolodziej A, Beltzer JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG63739 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Page 71; 115pp; English.
                                                  'label= Pro, Trp
                                                                                 /label= Trp, Tyr
                'label= His, Val
                                                                                                                                                                                        28-JUL-2000; 2000WO-US020612.
                                                                                                                                                                                                                         99US-0146425P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sest Local Similarity 100.0
                                                                                                                                                                                                                                                                        (EPIX-) EPIX MEDICAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Misc-difference 1. .10
                                                                                                                                                                                                                                                                                                                                           WPI; 2001-210995/21
                                                                                                                                                                                                                                                                                                                                                                                               thrombotic disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 XXXXC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 xxxxc 10
Misc-difference 7
                                                                   Misc-difference 9
                                                                                                                                                                                                                                                         (DYAX-) DYAX CORP
                                 Misc-difference 8
                                                                                                                     WO200109188-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10 AA;
                                                                                                                                                                                                                       29-JUL-1999;
                                                                                                                                                    08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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/note= "Xaa represent unspecified residues"

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ABG68465 standard; peptide; 10 AA.
                                                                          Example 7; Col 53; 108pp; English.
                                                                                                                                                                        Local Similarity 100.
hes 5; Conservative
                                            Clark RG, Lowman HB,
                                     (GETH ) GENENTECH INC
                                                    WPI; 2001-520042/57.
                                                                                                                                                                                   6 XXXXC 10
                                                                                                                                                                                           6 xxxxc 10
                                                                                                                                                             Sequence 10 AA;
                                                                                                                                                                                                                             07-OCT-2002
                      31-MAR-1998;
              26-JUN-2001.
                                                                                                                                                                                                                      ABG68465;
                                                                                                                                                                     Query Match
                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                       RESULT 19
                                                                                                                                                                                                          ABG68465
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The invention relates to treatment or prophylaxis (M1) of a subject having a disorder characterised by abnormal interaction of Grb7 (Growth Eator receptor-bound protein 7 and a Grb7 ligand, comparising administering to a subject in need of the treatment, a non-phosphorylated administering to a subject in need of the treatment, a non-phosphorylated peptide comprising a sequence (S1, Tyr-Ala-Asn, Tyr-Glu-Asn and Tyr-Asp-Crb of its functional equivalent, in an amount effective to inhibit the clisorder. Also included are peptide antagonists, an expression vector comprising consider acids encoding the artagonists, an expression vector comprising considered and a mount of the nucleic acid, a host cell transformed or transfered with the vector, screening (W2) a molecular library to identify a compound that inhibits increation between Grb7 and a peptide antagonist and a phage display increatment of a subject having a disorder characterised by abnormal conservation of Grb7 and a Grb7 ligand, including breast or oesophageal cancer, primary tumour or metastasis, or disorders in kinhey, liver, gonads, breast, oesophagus, pancreas, prostate, small intestine, colon, ovary, testes and lung. The present sequence is a generic example of a Grb7 peptide antagonist of the invention
                                                                                                                                                                                                                                                                                                                                                             Treatment or prophylaxis of a subject having a disorder characterized by abnormal interaction of Grb7 and a Grb7 ligand, involves administering to a non-phosphorylated peptide to a subject in need of the treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.0%; Score 13; DB 5; Length 10; 100.0%; Pred. No. 1.3e+04; rive 0; Mismatches 0; Indels
                                                                                                                                                                                              (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Page 120, 186pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG68462 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                     Oligino L;
                                                                               05-NOV-2001; 2001WO-US047400
                                                                                                                                   03-NOV-2000; 2000US-0245755P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
                                                                                                                                                                                                                                                                                                               WPI; 2002-547451/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                     Krag DN, Pero SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CXXXX 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CXXXX 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-OCT-2002
                        10-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG68462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4BG68462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence was used to construct a peptide library for identification of peptides which inhibit the binding of insulin-like growth factor (IGF)—I to IGF binding proteins (IGFBP). IGF agonist peptides are used to increase serum and tissue levels of IGF-1 in mammals with hyperglycemic, obesity-related, neurological, cardiac, anabolic renal or immunological disorders. They may also be used to increase whole body, bone and muscle growth rate in normal and hypopituitary animals, to protect body weight and nitrogen loss during catabolic states, kidney regenerative disorders and promote neuroprotection or repair following CNS damage or injury, to treat hypoxia, to promote wound healing, for cardiac regeneration, to reverse cancer cachexia, to inhibit or cagneration, to respendent action of growth hormone context growth hormone activity onset diabetes and adult growth hormone activity onset diabetes and vot treat specific IGF deficiency, to treat maturity onset diabetes and/or to treat specific IGF deficiency. They may also be used to treat growth-hormone resistant short stature, growth hormone insensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated peptides used to increase serum and tissue levels of insulin-
like growth factor in those with hyperglycemic, obesity-related,
neurological, cardiac, anabolic, renal or immunological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           syndrome, osteoporosis and catabolic states, and reduce obesity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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                                                                                                                                                                                                                                                                                                                                                    Robinson ICAF;
                                                                                                                                                                           98US-00052888.
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Gaps ..

Growth factor receptor-bound protein 7; Grb7; ligand; antagonist; cytostatic; cancer; phage display; tumour; metastasis; breast cancer; oesophageal cancer; kidney disorder; liver disorder; gonad disorder; breast disorder; sesophageal disorder; pancreatic disorder; proteit disorder; mall intestine disorder; placental disorder; colon disorder; litestine disorder; placental disorder; Growth factor receptor-bound protein 7 antagonist example #16. WO200236142-A2 10-MAY-2002. Synthetic. 

Growth factor receptor-bound protein 7; Grb7; ligand; antagonist; cytostatic; cancer; phage display; tumour; metastasis; breast cancer; ossophageal cancer; kidney disorder; liver disorder; gonad disorder; breast disorder; oseophageal disorder; pancrettic disorder; prostate disorder; small intestine disorder; placental disorder; colon disorder; ovary disorder; testicular disorder; lung disorder.

WO200236142-A2

Synthetic

Growth factor receptor-bound protein 7 antagonist example #19.

(first entry)

05-NOV-2001; 2001WO-US047400.

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A peptide useful for treating a IgB-mediated disease or disorder in a host e.g. allergic rhinitis, asthma, which competes with immunoglobulin E for binding to high affinity IgE receptor in an in vitro assay.
                                                                                                                                                                                                                                                   The present invention relates to a method for treating cartilage disorders. The method comprises contacting cartilage with an active agent disorders. The method comprises contacting cartilage with an active agent preference insulin-like growth factor (IGF-1) analog with a binding affinity preference for IGFBP-1, an IGF-1 analog with a binding affinity preference for IGFBP-1 over IGFBP-3, or a IGFBP displacer peptide that prevents the interaction of IGF with an IGFBP and does not bind to human IGF receptor. The method is useful for treating cartilage disorders (CD), including degenerative CD, articular CD such as rheumatoid arthritis and osteoarthritis. The present sequence
                                                                      Treating cartilage disorders including cartilage damage by injury or degenerative cartilagenous disorders, by contacting cartilage with insulin-like growth factor analog with altered affinity for IGF-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IgE receptor, immunoglobulin; FcepsilonRI; antagonist; phage display; protein co-ordinate data; IgE-mediated disease; allergic rhinitis; asthma; allergic asthma; allergic dermatitis; urticarid-angicedema; parastic infection; IgE myloma; immune-related disorder; inflammatory disorder; diabetes mellitus; reperfusion injury; stroke; IgE-mediated gastrointestinal inflammatory disease; burn; immune rejection of graft; myocardial infarction; atherosclerosis; acute lung injury; haemorrhagic shock; septic shock; acute tubular necrosis; endometriosis; degenerative joint disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.0%; Score 13; DB 5; Length 10; 100.0%; Pred. No. 1.3e+04; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Representative peptide of phage displayed g8 library 508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lowman HB, Reynolds ME, Nakamura GR, Starovasnik MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 was used to illustrate the invention
                                                                                                                                                                                                         Example 1; Page 40; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG66157 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-SEP-2001; 2001WO-US030289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-SEP-2000; 2000US-0235353P.
23-MAR-2001; 2001US-0278540P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 5; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-444016/47.
                            WPI; 2002-082942/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 XXXXC 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200226781-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pancreatitis.
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                                                                                                                                                      proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG66157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 22
ABG66157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to treatment or prophylaxis (MI) of a subject having a disorder characterised by abnormal interaction of Grb7 (Growth factor receptor-bound protein 7 and a Grb7 ligand, comprising disorder charactering to a subject in need of the treatment, a non-phosphorylated administering to a subject in need of the treatment, a non-phosphorylated peptide comprising a sequence (SI, Tyr-Ala-Asn, Tyr-Glu-Asn and Tyr-Asp-Asn) or its functional equivalent, in an amount effective to inhibit the disorder. Also included are peptide antagonists, an expression vector comprising the nucleic acid, a host cell transformed or transfected with the vector, creening (M2) a molecular library to identify a compound that inhibits interaction between Grb7 and a peptide antagonist and a phage display interaction between Grb7 and a peptide antagonist and a phage display interaction of Grb7 and a Grb7 ligand, including breast or ossophageal interaction of Grb7 and a Grb7 ligand, including breast or ossophageal cancer, primary tumour or metastasis, or disorders in kinhey, liver, gonads, breast, ossophagus pancreas, prostate, small intestine, generic example of a Grb7 peptide antagonist of the invention
                                                                                                                                                                                                                             Treatment or prophylaxis of a subject having a disorder characterized by abnormal interaction of Grb7 and a Grb7 ligand, involves administering to a non-phosphorylated peptide to a subject in need of the treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%; Score 13; DB 5; Length 10; 100.0%; Pred. No. 1.3e+04; ive 0; Mismatches 0; Indels
                                                                 (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide motif #10 used in peptide library.
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                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 118; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB57651 standard; peptide; 10 AA.
                                                                                                                         Krag DN, Pero SC, Oligino L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-MAY-2001; 2001WO-US015904.
                      03-NOV-2000; 2000US-0245755P.
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15-NOV-2000; 2000US-0248985P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                            WPI; 2002-547451/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 XXXXC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 xxxxc 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200187323-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB57651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 21
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The invention relates to a peptide which competes with immunoglobulin (Iq) E 134 comprising a sequence (S1), for binding the high affinity IgE receptor (FecepilonR1) in an in vitro assay and having a formula given in receptor (FecepilonR1) in an in vitro assay and having a formula given in the specification. Also included are a fusion protein comprising the peptide, a compound that mimics the three-dimensional surface structure of the peptide, a compound with a solvent accessible surface that mimics the solvent accessible surface that mimics the solvent accessible surface defined by the side of residues (R) for the solvent accessible surface for mimics the solvent accessible surface defined by the solvent accessible surface defined by the side of residues (R) for the solvent accessible surface for solvent accessible surface for solvent accessible surface for solvent accessible surface defined by the side of the mimics the coordinates of IgB134 a peptide with structural coordinates of IgB134 a peptide with structural coordinates of IgB134 residues (R). C) is useful for inhibiting the binding of IgB to high affinity IgE receptor. The peptide is useful for selecting a molecule which blocks the interaction of IgB with high affinity IgE receptor. The peptide is useful for selecting a molecule which blocks in the peptide is useful for treating of IgB mediated disease or disorder in a second processes such as IgE-dependent activation and degranulation of mast colls and basophils, as well as consequent release of inflammatory mediators such as Instamine. (C) is useful for treating an IgB mediated matching acceptor associated minimatory disorders, immune-release of uttercaria-angioedema, parasitic infection, IgE myeloma, immune-related disease of disorders, inflammatory stroke, mycoardial infection, and parting of the invention of the invention (or a library of peptides of the i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herpes virus infection; detection; therapy; zinc-finger motif; antiviral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.0%; Score 13; DB 5; Length 10; 100.0%; Pred. No. 1.3e+04; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gammaherpes virus subfamily zinc-finger motif.
Example 7; Page 100; 328pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE19557 standard; protein; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2. .4
/label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6. .9
/label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
(revised)
(first entry)
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Query Match
Best Local Similarity 100...
Best Local Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CXXXX 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CXXXX 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200204492-A2
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07-AUG-2003
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The invention relates to a method of detecting an agent for use in the treatment of herpes virus infection. The method comprises forming a herpes virus polypeptide/zinc complex, adding a test agent to the polypeptide/zinc complex, and detecting any change in the complex. The invention also relates to the use of known agents, such as 2,2'-dithiobisbenzamide (DIBA) and azodicarbonanide (ADA), and unknown agents for the manufacture of a medicament for the treatment of herpes virus infections. The method is useful for detecting agents for use in the treatment of herpes virus infection. The present sequence is Gammaherpes thus subfamily zinc-finger motif of herpes virus 1863 functional homologue. (Updated on 07-AUG-2003 to correct OS field.) (Updated on 29-AUG-2003 to strandardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytostatic, antidiabetic; osteopathic; vasotropic; tranquiliser; IGF-1; vulnerary; antidiasthmatic; ophthalmological; antagonise; ischemic injury; insulin-like growth hormone 1; IGF, cancer; diabetic; nephropathy; diabetic retinopathy; acromegaly; macular degeneration; trauma; asthma;
                                                                                                                                                                                               Detecting an agent useful for treating herpes virus infection comprises determining any change in a polypeptide/zinc complex in the presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 50.0%; Score 13; DB 5; Length 10; Best Local Similarity 100.0%; Pred. No. 1.3e+04; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insulin-like growth factor related peptide SEQ ID No 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schaffer ML, Sidhu SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABJ15256 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                       Claim 9; Page 29; 43pp; English.
                 11-JUL-2001, 2001WO-GB003114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAR-2002; 2002WO-US007606.
                                                     11-JUL-2000; 2000GB-00016890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAR-2001; 2001US-0275904P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JAN-2003 (first entry)
                                                                                                                          Clements JB, Maclean AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deshayes K, Lowman HB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC
                                                                                   (UNIU ) UNIV GLASGOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-732826/79.
                                                                                                                                                              WPI; 2002-226983/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CXXXX 5
                                                                                                                                                                                                                                     the test agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200272780-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABJ15256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 24
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                                                                                                   The invention relates to novel peptides that can antagonise the interaction of insulin-like growth hormone 1 (IGF-1). The peptides are useful for treating disorders such as cancer, diabetic complication accempated by IGF-1, e.g. diabetic retinopathy or nephropathy, acromegaly, age-related macular degeneration, ischemic injury or trauma. Other disorders that can be treated by the peptide include restenosis or asthma. This sequence represents a peptide relating to the IGF antagonist peptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label= Cys, OTHER
note= "OTHER = beta-mercaptopropionic acid or nothing"
New peptides antagonizing insulin-like growth factor (IGF), useful for treating disorder such as cancer, diabetic complication exacerbated by IGF-1, acromegaly, age-related macular degeneration, ischemic injury, trauma, asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cyclohexylalanine
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oxytocin; antiinflammatory; analgesic; antiallergic; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER
diaminobutyric acid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arg, OTHER
diaminobutyric acid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               when position 1 is beta-
                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              label= Tyr, Phe, OTHER nothing or nothing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide with oxytocin activity for use as antiinflammatory
                                                                                                                                                                                                                                                      Length 10;
                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Ile, Val, Phe, OTHER
/note= "OTHER = homophenylalanine,
nothing"
                                                                                                                                                                                                                                                      50.0%; Score 13; DB 5; Le
100.0%; Pred. No. 1.3e+04;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l. .6
/note= "when position 1 is Cys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   label= Ile, Leu, Val, Thr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tabel= Gln, Ser, Thr, Arg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "OTHER = homoserine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Gly, Ala, OTHER
/note= "OTHER = nothing"
10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "OTHER = nothing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "thioether bond,
mercaptopropionic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             citrulline or nothing'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              label= Pro, OTHER
                                                                               Disclosure; Page 65; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                       ABR41963 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nothing"
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dermatological; cyclic.
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                             6 XXXXC 10
                                                                                                                                                                                                                                                                                                                                     70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
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                                                                                                                                                                                                                               Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                     6 xxxxc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-AUG-2003
                                                                                                                                                                                                                                                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                  ABR41963;
                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                             RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                           ABR41963
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/label= Cys, CTHER
/note= "OTHER = Mpa (beta-mercaptopropionic acid); may or
may not be present; linked to Cys at position 6 via CH2-S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present"
                                                                                                                                                                                                                                                                                                   The present sequence is a generic sequence for peptides of the invention (see also ABR41964-86) that have oxytocin activity and are useful in pharmaceutical compositions for treatment of inflammation, e.g. oedema, hyperalgesia, myeloperoxidase accumulation, cystitis, pancreatitis, cutaneous inflammation, allergic thinitis, dermatitis, airway inflammation, and asthma (all claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Gln, Ser, Thr, Arg, OTHER
/note= "OTHER = Cit (citrulline), Daba (Diaminobutyric
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                            ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 not be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= lle, Val, Phe, OTHER
/note= "OTHER = Hoph (homophenylalanine), Cha
(cyclohexylalanine); may or may not be present"
                                                                                                                                                                                                                                         Use of substances with oxytocin activity for the preparation of pharmaceutical composition against inflammation e.g. edema.
                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Tyr, Phe, OTHER
/note= "OTHER = O-methyl-Tyr; may or may
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant growth stimulant; germination; oxytocin.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
/note= "C-terminal amide"
                                    nothing"
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 13;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE36134 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide with oxytocin activity #1.
                          OTHER
                                                                                                                                                                                                                                                                                                                                                                                                          50.0%; Scc.
100.0%; Pre
                                                                                                                                                                                                                                                                                 Claim 3; Page 56; 78pp; English.
                       /label= Gly, OTH
/note= "OTHER =
                                                                                                                                                                                              Uvnaes-Moberg K, Lundeberg T;
                                                                                                                                   31-AUG-2001; 2001SE-00002910
                                                                                                           02-SEP-2002; 2002WO-SE001560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
                                                                                                                                                            (UVNA/) UVNAES-MOBERG K.
(LUND/) LUNDEBERG T.
                                                                                                                                                                                                                      WPI; 2003-371695/35.
                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
               Misc-difference 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 CXXXX 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10 AA;
                                                              WO2003017922-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CXXXX
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                                                                                      06-MAR-2003
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Matches
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The invention relates to the use of substances with oxytocin activity for the preparation of a pharmaceutical composition for the treatment of cancer in situ and cervicitis. The cancer in situ and cervicitis include diseases in vagina and cervix originating from infections as well as inflammations. The cancer in situ is related to cervix and also includes precancerous disease states, squamous cell carcinoma and koilocytosis due to the herpes virus. The present sequence is a peptide with oxytocin
                                                                                                           note= "This residue is linked to Xaa at position 1 via
                                 /label= Gln, Ser, Thr, Arg, OTHER
/note≈ "OTHER = Cit (citrulline), Daba (Diaminobutyric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New use of at least one substance comprising a polypeptide derivative with oxytocin activity for the preparation of a pharmaceutical composition for the treatment of cancer in situ and cervicitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                   HOB
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                                                                                                                                                                                                                                                                                             /note≈ "Optionally Gly; C-terminal amide"
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                                                                                                                                                                                                   'note≈ "Optionally lle, Leu, Val,
(homoserine), Cit, Daba"
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100.0%; Pred. No. 1.3e+04;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                           note≈ "Optionally Gly or Ala"
Phe, Cha (cyclohexylalanine)"
                                                                                                                                                               note≈ "Optionally Pro"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 20; 41pp; English.
                                                                                                                           CH2-S-S linkage'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Uvnaes-Moberg K, Lundeberg T;
                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2001; 2001SE-0000684
                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2002; 2002WO-SE000362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UVNA/) UVNAES-MOBERG K.
                                                                     acid) "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-029847/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LUND/) LUNDEBERG T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 5, Conserv
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                   Misc-difference
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                                                                                                                                                                                                                                                                                                                                 WO200267974-A1
                                                                                                                                                                                                                                                                                                                                                                     06-SEP-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to the use of a substance with oxytocin activity in order to stimulate plant growth, dormancy breaking and germination. The present sequence is a peptide with oxytocin activity
                               note= "This residue is linked to Xaa at position 1 via
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Optionally Cys, Mpa (beta- mercaptopropionic acid); linked to Cys at position 6 via CH2-S-S linkage"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of a substance with oxytocin activity to stimulate plant growth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oxytocin; cancer; cervicitis; infection; squamous cell carcinoma;
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                                                                                                                                             Daba"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.0%; Score 13; DB 6; Length 10; 100.0%; Pred. No. 1.3e+04; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                   /note= "Optionally Gly; C-terminal amide"
                                                                                                                       /label= Ile, Leu, Val, Thr, Arg, OTHER
(note= "OTHER = Hos (homoserine), Cit,
                                                                                                                                                                                                   note= "May or may not be present"
                                                                                     note= "Optionally Pro"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dormancy breaking and germination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide #1 with oxytocin activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE30352 standard; peptide; 10 AA.
                                                   CH2-S-S linkage"
                                                                                                                                                                               /label= Gly, Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 19; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Uvnaes-Moberg K, Lundegardh B;
                                                                                                                                                                                                                                                                                                                                                                                   19-JUN-2001; 2001SE-00002185.
                                                                                                                                                                                                                                                                                                                                                 19-JUN-2002; 2002WO-SE001208
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Best Local Similarity
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KW blood glucose level; hyperglycaemic disorder; obesity-related disorder;
KW neurological disorder; cardiac disorder; anabolic disorder;
KW renal disorder; immunological disorder; anabolic disorder;
KX Synthetic.

XX Synthetic.

XX D14-OCT-2003.

XX PF 28-NOV-2000; 2000US-00723547.

XX PF 28-NOV-2000; 2000US-00723547.

XX PF 28-NOV-2000; 2000US-00723547.

XX O4-APR-1999; 97US-00825852.

PR 31-MAR-1998; 98US-0052888.

XX GETH ) GENENTECH INC.

XX Clark RG, Lowman HB, Robinson ICAF;

XX Clark RG, Lowman HB, Robinson ICAF;

XX Clark RG, Lowman HB, Robinson ICAF;

XX TIOCTEASING Servum and Lissue levels of biologically active insulin-like PT growth factor (IGF)-I in a mammal for treating e.g. renal disorder, by administering IGF peptide.
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Example 7; SEQ ID NO 35; 117pp; English.

The invention relates to a method for increasing serum and tissue levels of biologically active insulin-like growth factor I (IGF-I) in a mammal comprising administering a growth hormone, a growth hormone releasing peptide, a growth hormone releasing hormone, a growth hormone binding secretagogue, a growth hormone in combination with growth hormone binding protein, an IGF in combination with an IGF binding protein, an IGF in combination with an IGF binding protein, and glucose levels in a mammal. The method is useful for increasing serum and tissue levels of biologically active IGF-I in a mammal for treating hyperglycaemic, obesity-related, neurological, cardiac, anabolic, repal or immunological disorders. This sequence represents a peptide used in the method of the invention.

Sequence 10 AA;

Query Match 50.0%; Score 13; DB 7; Length 10; Best Local Similarity 100.0%; Pred. No. 1.30+04; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps

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6 XXXXC 10 ||||| 6 XXXXC 10

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Search completed: May 4, 2004, 06:52:04 Job time : 53 secs

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US-09-248 519-1.

Sequence 21, Application US/09284819

Patent No. 6365712

GENERAL INFORMATION:
APPLICANT: Kelly, Kathleen
APPLICANT: Kelly, Kathleen
APPLICANT: Rely, Kathleen
APPLICANT: The Government of the United States of America
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Methods and Compositions for Inhibiting Inflammation
TITLE OF INVENTION: Methods and Compositions for Inhibiting Inflammation
TITLE OF INVENTION: Methods and Compositions for Inhibiting Inflammation
TITLE OF INVENTION: Wombar: US/09/284,819
CURRENT APPLICATION NUMBER: US 60/027,871

FARLIER APPLICATION NUMBER: US 60/027,871

EARLIER PILING DATE: 1999-10-25

NUMBER OF SEQ ID NOS: 21

SEQ ID NO 21

LENGTH: 12

CORTWARE: PatentIn Ver. 2.1

LENGTH: 12

CORGANISM: Artificial Sequence
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ALIGNMENTS
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                           4, 2004, 07:10:30 ; Search time 23 Seconds (without alignments) 22.446 Million cell updates/sec
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/cgn2_6/ptcdata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptcdata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptcdata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptcdata/2/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptcdata/2/jaa/PCTUS_COMB.pep:*
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-326-039-21
US-08-991-970A-17
US-08-991-970A-17
US-09-326-039-115
US-09-326-039-115
US-09-326-039-115
US-08-821-988-45
US-08-821-988-45
US-08-821-988-45
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US-09-52-888-31
US-09-723-91-31
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Maximum Match 100%
Listing first 250 summaries
                                                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
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APPLICANT: Sprugel, Katherine H.
APPLICANT: Sprugel, Katherine H.
APPLICANT: Sprugel, Katherine H.
APPLICANT: Sprugel, Katherine H.
APPLICANT: Ren, Hong Ping
APPLICANT: Hoffmat, Ross C.
APPLICANT: Hoffmat, Ross C.
APPLICANT: Conklin, Darrell C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: STIMULATING PANCREATIC ISLET CELL REGENERATION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CONTY: Scattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 26; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 10; Conservative 0; Mismatches 0; Indels
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COTHER INFORMATION: Xaa is any amino acid except Cys US-08-950-720A.17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,890
FILING DATE:
CLASSIFICATION:
FastSEQ for Windows Version 2.0
  SOFTWARE: FABLSEQ for Windows Vers:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,720A
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APPLICATION NUMBER: 60/033,003
FILING DATE: December 16, 1996
ATTORNEY AGENT INFORMATION:
NAME: Sawislak, Deborah A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/08991890 Patent No. 6114307
                                                                                                CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sawishlak, Deborah A REFERENCE/DOCKET NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-0
TELECHONE: 206-442-6672
TELEPHONE: 206-442-6672
TELEPAX: 206-442-6673
TELEPAX: 206-442-6673
TELEPAX: 106-442-6673
TELEPAX: 206-442-6673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: No. 6046028e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
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US-08-991-890-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: VARIANT

1 LOCATION: (0) ...(0)

7 OTHER INFORMATION: Xaa is any amino acid residue except for cysteine.

US-09-326-039-21
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FEATURE:
CTHER INFORMATION: Description of Artificial Sequence: Asp/Asn OTHER INFORMATION: Deta-hydroxylation consensus motif
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)...(12)
CTHER INFORMATION: Xaa = any amino acid
US-09-284-819-21
                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 26; DB 3; Length 14; Best Local Similarity 100.0%; Pred. No. 7.9; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: CONKlin, Darrell
TITLE OF INVENTION: Disulfide Core Polypeptides
FILE REPRENCE: 98-13
CURRENT APPLICATION NUMBER: US/09/326,039
CURRENT FILING DATE: 1999-06-04
EARLIER FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 23
NOTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 21
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17, Application US/08950720A; Patent No. 6046028; GENERAL INFORMATION; APPLICANT: Conklin, Darrell C. APPLICANT: Lofton-Day, Catherine E. APPLICANT: Lofton-Day, Catherine E. APPLICANT: Lofton-Day, Catherine E. APPLICANT: Lofton-Day, Catherine E. TITLE OF INVENTION: INSULIN HOMOLOG NUMBER OF SEQUENCES: ADDRESSEE: ZymoGenetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21, Application US/09326039 Patent No. 6239254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CXXXXXXXXX 10
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
US-08-950-720A-17
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us-10-046-922-33.open.rai

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Sequence 157, Application US/10158847

Sequence 157, Application US/10158847

Patent No. 6592865

GENERAL INFORMATION:

TILLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity

TILLE OF INVENTION: MARBER: US/10/158,847

CURRENT APPLICATION NUMBER: US/10/158,847

CURRENT FILING DATE: 2002-06-03

PRIOR APPLICATION NUMBER: 60/295,004

PRIOR APPLICATION NUMBER: 60/295,004

PRIOR SPILOR APPLICATION NUMBER: 60/295,004

NUMBER OF SEQ ID NOS: 158

SOFTWARE: PARTON NOS: 158

SOFTWARE: PARTON NOS: 158

LENGTH: 16

TYPE: RT

OCCANION: (1).-(3)

OTHER INFORMATION: X equals any amino acid

PERTURE:

NAME/KEY: MISC_FEATURE

LOCATION: (5).-(12)

OTHER INFORMATION: X equals any amino acid

PERTURE:

NAME/KEY: MISC_FEATURE

LOCATION: (5).-(12)

OTHER INFORMATION: X equals any amino acid

PERTURE:

NAME/KEY: MISC_FEATURE

LOCATION: (5).-(12)

OTHER INFORMATION: X equals any amino acid

PERTURE:

NAME/KEY: MISC_FEATURE

LOCATION: (5).-(12)

OTHER INFORMATION: X equals any amino acid

PERTURE:

NAME/KEY: MISC_FEATURE

NAME/KEY: MISC_FEATURE

LOCATION: (5).-(12)

NAME/KEY: MISC_FEATURE

NAME/KEY: MISC_FEATURE

NAME/KEY: MISC_FEATURE

LOCATION: (5).-(12)

NAME/KEY: MISC_FEATURE

NAME/KEY: MISC_FEATURE
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100.0%; Score 26; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 26; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                     NAME/KEY: SITE
LOCATION: (11)
OTHER INFORMATION: Xaa=Leu, lle, Val, Met, or Phe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTHER INFORMATION: X equals any amino acid US-10-158-847-157
                       LOCATION: (10)
OTHER INFORMATION: Xaa=any amino acid
                                                                                                                                                                                   FRATURE:
NAME/KEY: SITE
LOCATION: (12)
OTHER INFORMATION: Xaa=any amino acid
                                                                                                                                                                                                                                                                                                  FEATURE:
NAMB/KEY: SITE
LOCATION: (13)
OTHER INFORMATION: Xaa=any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: SITE
1. LOCATION: (14)
7. UCRATION: (14)
7. UTER INFORMATION: Xaa=any amino acid
US-09-201-226-3
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LOCATION: (14)..(16)
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US-09-326-039-19
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Sequence 3, Application US/09201226

Sequence 3, Application US/09201226

Patent NO. 6135942

Patent NO. 6135942

Patent NO. 6135942

TITLE OF INVENTION: WUCLEIC ACIDS AND PROTEINS OF A D. MELANOGASTER

TITLE OF INVENTION: WUCLEIC ACIDS AND USES THEREOF

TITLE OF INVENTION: WUSELIN-LIKE GENE AND USES THEREOF

FILE REFERENCE: 7326-077

CURRENT PAPLICATION NUMBER: US/09/201,226

CURRENT FILING DATE: 1998-11-30

NUMBER OF SEQ 1D NOS: 3

SOFTWARE: Patentin Ver. 2.0

SEQ 1D NO 3

LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 3...5
CHER INFORMATION: Xaa is any amino acid except Cys
NAME/KEY: Other
CATION: 7...14
COTHER INFORMATION: Xaa is any amino acid except Cys
US-08-991-890-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: SITE
LOCATION: (3)
OTHER INFORMATION: Xaa=any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: SITE
LOCATION: (4)
OTHER INFORMATION: Xaa=any amino acid
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NAME/KEY: SITE
LOCATION: (7)
OTHER INFORMATION: Xaa=any amino acid
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LOCATION: (5)
OTHER INFORMATION: Xaa=any amino acid
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OTHER INFORMATION: Xaa=any amino acid
FEATURE:
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LOCATION: (9)
OTHER INFORMATION: Xaa=any amino acid
FEATURE:
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-41
TELECOMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                    INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Other
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GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: RAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: THORN, Judith M.
APPLICANT: POWLKS, Dana M.
APPLICANT: FOWLKS, Dana M.
APPLICANT: FOWLKS, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: 1801ARING PEPTIDES AND METHODS OF TITLE OF INVENTION: 1801ARING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                            100.0%; Score 26; DB 4; Length 18; larity 100.0%; Pred. No. 8.7; Conservative 0; Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/602,999A
FILING DATE: 16-FEB-196
CLASSIFICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-196
ATTORNEY/AGENT INFORMATION:
NAME: MISTORIA, S. Leslie
REGISTRATION NUMBER: 18,872
REPRENCE/DOCKET UNBER: 1101-202
TELEPHONE: (212) 869-9741/8864
TELEPHONE: (212) 869-9741/8864
TELEPHONE: (212) 869-9741/8864
TELEPHONE: GHARACTERISTICS:
LENGTH: 19 anino acids
TVENCYMENT APPLICATION INCOMPATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 anino acids
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100.0%; Score 26; DB 3
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                       US-08-602-999A-35; Sequence 35, Application US/08602999A; Patent No. 6184205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 35, Application US/08278865
Patent No. 6303574
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
US-08-602-999A-35
                                                                                                                                                                  1 CXXXXXXXC 10
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                                                          Ouery Match
Best Local Similarity
Matches 10; Conserv
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US-08-278-865-35
           US-08-821-498-45
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Patent No. 6326155
GENERAL INFORMATION:
APPLICANT: MACLENNAN, John M
APPLICANT: LADNER, Robert C
TITLE OF INVENTION: Engineering Affinity Ligands for Macromolecules
NUMBER OF SECUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSE: Banner & Witcoff, Ltd.
STREET: 75 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAMB/KEY: VARIANT
LOCATION: (0) ...(0)

CTHER INFORMATION: Xaa is any amino acid residue except for cysteine.
US-09-326-039-19
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MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage COMPUTER: IBM PC Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Microsoft Word 6.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/821,498
FILING DATE: 20-March-1997
CLASSIFICATION: PRIOR APPLICATION NUMBER: 08/619,885
FILING DATE: 20-March-1996
ATTORNEY/AGENT INFORMATION: NAME: YANKWICH, Leon R FILING DATE: 20-March-1996
ATTORNEY/AGENT INFORMATION: NAME: YANKWICH, Leon R REGISTRATION NUMBER: DYX-1CIP US REGISTRATION NUMBER: DYX-1CIP US TELECOMMINICATION HYDORMATION: TELECOMMINICATION HYDORMATION: TELECOMMINICATION HYDORMATION: TELECOMMINICATION HYDORMATION: TELEPHONE: 617-345-9101
INFORMATION FOR SEQ ID NO: 45: SEQUENCE CHARACTERICATICS: LENGTH: 18 amino acids TYPE: amino acids TYPE: amino acid STRANDEDNESS: single
Sequence 19, Application US/09126039
Patent No. 6219284
GENERAL INFORMATION:
APPLICANT: CORKLIN, Darrell
TITLE OF INVENTION: Disulfide Core Polypeptides
TITLE OF INVENTION: Disulfide Core Polypeptides
TITLE OF INVENTION: Disulfide Core Polypeptides
CURRENT APPLICATION NUMBER: US/09/326,039
CURRENT APPLICATION NUMBER: US/09/326,039
CURRENT FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FASISEQ for Windows Version 3.0
SEQ ID NO 19
LENGTH: 17
TYPE: RRT
CORANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 26; DB 3; Best Local Similarity 100.0%; Pred. No. 8.5; Matches 10; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Massachusetts
COUNTRY: United States of America
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
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Gaps .. 0

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##SBULL 1.15

| Sequence 31, Application US/08825852 |
| Patent No. 221146 |
| APPLICANT: Lowanan, Henry B |
| APPLICANT: Lowanan, Henry B |
| APPLICANT: Lowanan, Henry B |
| APPLICANT: Robinson, Iain C.A.F. |
| TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules |
| NUMBER OF SEQUENCES: 79 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: EN PC compatible
COMPUTER: Floppy disk
COMPUTER: Patent in PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURSIT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FLING DATE: 08/602,999
FLING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: MASTOCK, S. Leslie
FELING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: MASTOCK, S. Leslie
REGISTRATION NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 26; DB 4 100.0%; Pred. No. 8.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein FRAGMENT TYPE: N-terminal
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Best Local Similarity 100.
Matches 10; Conservative
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TOPOLOGY: unknow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-500-124-35
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APPLICANT: KAY, BRIAN K.
APPLICANT: FRAPES, ANDREW B.
APPLICANT: FINDRA, JUNEBNE A.
APPLICANT: GUILLIAM, LAMRENCE A.
APPLICANT: GUILLIAM, LAMRENCE A.
APPLICANT: DER, CANNING B.
TITLE OF INVENTION: STC SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: ISOLATING AND USING SAME
CORRESSED OBLOWERS: 106
CORRESSED OBLOWERS: 106
CORRESSED OBLOW, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSED: OBLOW, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSED: OBLOW, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSED: OBLOW, SPIVAK, MCCLELLAND, WAIER & NEUSTADT, ADDRESSED: OBLOW, SPIVAK, MCCLELLAND, WAIER & NEUSTADT, ADDRESSED: OBLOW, SPIVAK, MCCLELLAND, WAIER & NEUSTADT, STREET: VISGINIA
CONDUTER: U.S.A.
ZIP: 22202
COMUTER: ID PC COMPATION
STREET: VISGINIA
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COTWARE: PATENTION DATA:
COMPUTER: BATCATION DATA:
APPLICATION NUMBER: US/08/278,865
FILING DATE:
CLARRATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LEMERA: 24865 OPAT UR
INFORMATION FOR SEQ ID NO: 35:
LEMERA: LAMBOR ACIDE CHARACTERISTICS:
LEMERA: LAMBOR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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Sequence 35, Application US/09500124

Patent No. 6432920

GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: THORN, Judith M.
APPLICANT: POWLKES, Dana M.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James B.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467

CORRESPONDENCE ADDRESS:
ADDRESSESSIONATE ADDRESS:
ADDRESSESSIONATE ADDRESS:
ADDRESSESSIONATE ADDRESSIONATE ADDR
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STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
STATE: New York
ZIATE: New York
ZIP: 10.5.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein;
FRACMENT TYPE: N-terminal
US-08-278-865-35
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Best Local Similarity 100.
Matches 10; Conservative
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US-09-500-124-35
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Gaps

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CORRESPONDENCE ADDRESS:
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US-09-723-901-31
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                                                                                                                                                                                                                                                                                                                    Sequence 31, Application US/09052888
Patent No. 6251865
GENERAL INFORMATION:
APPLICANT: Clark, Ross Gl
APPLICANT: Lowman, Henry B.
APPLICANT: Exchinoson, Tain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
ADDRESSEE: Generhech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 31, Application US/09723890
Patent No. 6608031
GENERAL INFORMATION:
APPLICANT: Clark, Ross Gl
Lowman, Henry B.
Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 26; DB 3; Length 20; 100.0%; Pred. No. 9;
                                                                                                  DB 3; Length 20;
                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                           0; Mismatches
                                                                                                    100.0%; Score 26; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Winheath (Generical)
SOFTWARE: Winheath (Generical)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,888
FILING DATE: 31-Mar-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REGISTRATION NUMBER: 28,616
REFERNCE/DOCKET NUMBER: P1071P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 20 amino acids
Amino Acid
  : 20 amino acids
Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                  Query Match
Best Local Similarity 100.
Matches 10; Conservative
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TOPOLOGY:
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                        ; TYPE: Ami
; TOPOLOGY:
US-08-825-852-31
                                                                                                                                                                                                                                                                                       RESULT 13
US-09-052-888-31
    LENGIH:
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Lowman, Henry B.

Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA May
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Clark, Ross G1

Lowman, Henry B.

Lowman, Henry B.

Robinson, Ialn C.A.F.

TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules NUMBER OF SEQUENCES: 109

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way

CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
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                                                                                                                                                                                                                                                                                                                                                                                                                         ZIF: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/724,127
FILING DATE: 28-NO. 6635619-2000
CLASSIFICATION: «UNKNOWN:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/052,888
FILING DATE: 31-Mar-1998
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 28,616
REGISTRATION NUMBER: P1071P1
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
                                                                                                         Sequence 31, Application US/09724127
Patent No. 6635619
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 31, Application US/09723931
Patent No. 6645775
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 10; Conservative
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6 CXXXXXXXX 15
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US-09-723-931-31
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Lowman, Henry B.
Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/723,547
FILING DATE: 28-No. 6632794-2000
CLASSIFICATION: cUbknown>
PRIOR APPLICATION: CUbknown>
APPLICATION NUMBER: 09/052,888
FILING DATE: cUbknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 26; DB 4; Best Local Similarity 100.0%; Pred. No. 9; Matches 10; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Hasak, Janet E.
REGISTANTON WUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
                                      REFERENCE/DOCKET NUMBER: P1071P1
TELECOMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEPAX: 650/952-9881
INFORMATION FOR EGO ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: Linear SEQ ID NO: 31: US-09-723-547-31
                                                                                                                                                                                                                            TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way CITY: South San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 31, Application US/09723547; Patent No. 6632794; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650/952-9881
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                         TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                        1 CXXXXXXXC 10
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APPLICANT: Clark, Ross Gl
Lowman, Henry B.
Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                            Gaps
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                                                                                                                                                                            Indels
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible COMPUTER: 1BM PC compatible COERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Windatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/724,114
FILING DATE: 28-No. 6680298-2000
CLASSIFICATION: «Unknown>
PRIOR APPLICATION NUMBER: 09/052,888
ATTORNEY/ABCATION NUMBER: 09/052,888
FILING DATE: 31-Mar-1998
ATTORNEY/ABCAT INFORMATION:
REGISTRATION NUMBER: 28,616
REGISTRATION NUMBER: 28,616
TELECOMMUNICATION INFORMATION:
TELEBECOMMUNICATION INFORMATION:
TELEBECOMMUNICATION INFORMATION:
TELEBECOMMUNICATION INFORMATION:
TELEBECOMMUNICATION INFORMATION:
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                                                                                                                             Score 26; DB 4;
Pred. No. 9;
; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; SEQUENCE DESCRIPTION: SEQ ID NO: 31: US-09-724-114-31
                                            TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 31, Application US/09723913; Patent No. 6683053; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       Sequence 31, Application US/09724114
Patent No. 6680298
GENERAL INFORMATION:
LENGTH: 20 amino acids
TYPE: Amino Acid
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INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                               Query Match

Best Local Similarity 100.0%;

Matches 10; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-723-913-31
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US-09-723-873-33
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Sequence 31, Application US/09723873
Patent No. 6677305
GENERAL INFORMATION:
Clark, Ross Gl
Lowman, Henry B.
Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 26; DB 4; Length 20; 100.0%; Pred. No. 9; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC comparible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winbatin (Genentech) CURRENT APPLICATION DAIR:
APPLICATION NUMBER: US/09/723,873
FILING DATE: 28-No. 6677305-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/052,888
FILING DATE: 31-Mar-1998
ATTORNEY/AGENT INPORMATION:
NAME: HABSAK, Janet E.
REGISTRATION NUMBER: 28,616
                CORPUTER TANDELS TORM:
COMPUTER: 13.5 Inch, 1.44 Mb floppy disk
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WINPATIN (Geneticch)
CURRENT APPLICATION DATA:
FILING DATE: 28-No. 6645775-2000
CLASSIFICATION NUMBER: US/09/723,931
FILING DATE: 31-Mar-1998
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTATION UNMBER: 28,616
REFERENCE/DOCKET NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 28,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P1071P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: Linear SEQ ID NO: 31: US-09-723-931-31
                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 650/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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US-09-723-873-31
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Gaps
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                                                                                                                                                                                                                        DB 2; Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 23
US-09-130-225-5
Sequence 5, Application US/09130225
Sequence 5, Application US/09130225
Sequence 5, Application US/09130225
SEGUENCE INFORMATION:
APPLICANT: Mocked W.
APPLICANT: KOVESHION:
TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STRTE: Illinios
COUNTRY: USA
                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,225
FILING DATE:
                                                                                                                                                                                                                      Query Match
100.0%; Score 26; DB 2
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 24
US-00-455-061-5
Sequence 5, Application US/09455061
Setent No. 6329190
GENERAL INFORMATION:
APPLICANT: Wickham, Thomas J.
APPLICANT: Roelvink, Petrus W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 8-701124
FILING DATE: 21-AUG-1996
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
FILING DATE: 21-AUG-195
INFORMATION FOR SEQ ID NO:
SEQUENCE FOR CHARACTERISTICS:
LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear;
MOLECULE TYPE: peptide
US-09-130-225-5
                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                 , MOLECULE TYPE: peptide US-08-701-124-5
                                                                                                                                                                                                                                                                                                              1 CXXXXXXX 10
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                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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                     TITLE OF INVENTION: Inaula C.A.F.
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
ADDRESSE: Generich, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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100.0%; Score 26; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 9;

Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
CORPUTER: 1BM PC compatible
CORPUTER: 1BM PC compatible
CORPUTER: 1BM PC compatible
CORPUTER: 28-No. 1059/N23,913
FILING DATE: 28-No. 6683053-2000
CLASSIFICATION NUMBER: 08/09/723,913
FILING DATE: 28-No. 6683053-2000
CLASSIFICATION: «Unknown>
PRIOR APPLICATION NUMBER: 09/052,888
ATTONBEY AGENT INFORMATION:
NAMME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REGISTRATION NUMBER: 28,616
REGISTRATION NUMBER: 28,616
TELECOMMUNICATION NUMBER: 28,616
TELECOMMUNICATION NUMBER: 19071P1
TELECOMMUNICATION NUMBER: 20,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INCORATION:
APPLICANT Wickham, Thomas J.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Roelvink, Detrus W.
TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 31: US-09-723-913-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 22
US-08-701-124-5
; Sequence-5, Application US/08701124
; Patent No. 5846/782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 20 amino acids
TYPE: Amino Acid
    APPLICANT: Clark, Ross Gl
Lowman, Henry B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CXXXXXXXC 10
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Gaps
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NAMBER: US/09/969,192

FILING DATE: 01-Oct-2001

PRIOR APPLICATION DATA:

APPLICATION NAMBER: US 9-130225

FILING DATE: 06-DEC-1999

APPLICATION NUMBER: US 9-130225

FILING DATE: 06-AUG-1996

APPLICATION NUMBER: US 8-701124

FILING DATE: 11-AUG-1996
                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 26; DB 4; Length 23; 100.0%; Pred. No. 9.5; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: WICKHAM, THOMAS J.
ROELVINK, PETRUS W.
KOVESDI, INRE
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
CONSTRAINED PEPTIDE MOTIFS
NUMBER OF SEQUENCES: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
RADRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Hefner, M. Daniel
REGISTRATION NUMBER: 41,826
REFERENCE/DOCKET NUMBER: 213564
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
COATION: (9)..(13)
OTHER INFORMATION: Variable amino acid
NAME/KEY: MOD RES
LOCATION: (15)..(22)
OTHER INFORMATION: Variable amino acid
US-08-884-1569A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09969192
Patent No. 6649407
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%;
Matches 10; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                        1 CXXXXXXXX 10
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US-09-969-192-5
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                                                                                                                                                                                                                                                                                                                  임
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APPLICANT: CHIANG, MING-KO
APPLICANT: CHIANG, MING-KO
APPLICANT: FLANAGAN, JOHN G.
TITLE OF INVENTION: RECEPTOR TYROSINE PHOSPHATASE, AND USES RELATED THERETO
TITLE OF INVENTION: RECEPTOR TYROSINE PHOSPHATASE, AND USES RELATED THERETO
TITLE REFERENCE: HWY-020.01
CURRENT APPLICATION WUMBER: US/08/884,569A
CURRENT FILING DATE: 1997-06-27
PRIOR FILING DATE: 1996-07-02
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.1
SSQ ID NO 9
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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NAME/KEX: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
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Kovesdi, Imre
/ENTION: TARGETING ADENOVIRUS WITH USE OF
/ENTION: CONSTRAINED PEPTIDE MOTIFS
                                                                                                                                                                                                                                                                                   MEDIUM TYPE: FIDOPY disk
COMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/455,061
FILING DATE: 0.6-DEC-1999
PRIOR APPLICATION NUMBER: US 9-13025
FILING DATE: 0.6-DEC-1998
PRIOR APPLICATION NUMBER: US 8-701124
FILING DATE: 1.6-AUG-1996
ATTORNEY/AGENT INPORMATION:
NAME: Hefner, M Daniel
RESTRATION NUMBER: 41,826
REFERENCE/DOCKET NUMBER: 2.31302
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTER. 2.1333
                    TITLE OF INVENTION: TARGETING ADENOVIRUS WITH TITLE OF INVENTION: CONSTRAINED PEFTIDE MOTIFS NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 9
Matches 10; Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (2)...(7)
OTHER INFORMATION: Variable amino acid
NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08884569A
Patent No. 6399326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-455-061-5
                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CXXXXXXXX 10
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us-10-046-922-33.open.rai

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APPLICANT: SPARKS, ANDREW B.
APPLICANT: SPARKS, ANDREW B.
APPLICANT: THORN, JUDITH M.
APPLICANT: THORN, JUDITH M.
APPLICANT: DER, CHANNING J.
TITLE OF INVENTION: Src SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: SOLDATING AND USING SAME NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Alington
STARE: Virginia
STARE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 26; DB 3; Length 28; 100.0%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MUDIUM TYPE: Floppy disk
COMPUTER: IBW PC Compatible
OPERATING SYSTEM: PC-D0S/MS-DOS
SOFTWARE: PETENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKST NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEFAX: (212) 869-9741/8864
TELEFAX: (214) PENNIE
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LEBOTH: 28 amino acids
TYPE: amino acids
TYPE: amino acids
TOPPLICATION INCREDICED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopped disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SURRENT PEPTICATION DATE:
CLASSIFICATION NUMBER: US/08/278,865
FILING DATE:
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: Villacorta, Gilberto M.
REGISTRATION NUMBER: 34,038
REPERBENCE/DOCKET NUMBER: 4980-007-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 36, Application US/08278865
Patent No. 6303574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CXXXXXXX 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-602-999A-36
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US-08-278-865-36
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Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPAKES, Andrew B.
APPLICANT: THORN, Judith M.
APPLICANT: THORN, Judith M.
APPLICANT: POWLKES, Dana M.
APPLICANT: POWLKES, Dana M.
APPLICANT: FOWLKES, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: 1SOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 10; Conservative 0; Mismatches 0; Indels
     Sequence 95, Application US/08179481

Sequence 15, Application US/08179481

Patent No. 5624816

GENERAL INFORMATION:

APPLICANT: CARCAHRES CARRAWAY, CORALIE A.

APPLICANT: CARCAHRES CARRAWAY, CORALIE A.

APPLICANT: CARCAHRES CARRAWAY, CORALIE A.

APPLICANT: FREGIEN, NEVIS L.

TITLE OF INVENTION: ONCOGENE PRODUCT LIGAND
NUMBER OF SEQUENCES: 125

CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHWAN, DARBY & CUSHWAN
STREET: 1100 NEW YORK AVENUE, N.W.

CITY: WASHINGTON
STRATE: D.C.

COUNTRY: U.S.A.

ZITP: 20005-3918

COUNTRY: U.S.A.

ZITP: 20005-3918

CONTYER: IBM PC COMPACINE
MEDIUM TYPE: Floppy disk
CONTYTER: IBM PC COMPACINE

MEDIUM TYPE: Floppy disk
CONTYTER: BAPELICATION DATA:

APPLICATION NUMBER: US 07/922,521

FILING DATE: 28-DEC-1993

CREASIFICATION NUMBER: US 07/922,521

FILING DATE: 30-UUL-1992

ATTORNEY/AGENT INFORMATION:

FELEPHONE: (202) 822-0944

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHRACTERISTICS:

LENGTH: 24 amino acids

TELERAL ANTERNES: single

TOTAL ANTERNES: Single

TOTAL ANTERNES: Single

TOTAL ANTERNES: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CXXXXXXXX 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 CXXXXXXXC 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS-08-602-999A-36
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Gaps

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RESULT 31
US-08-478-112-19
US-08-478-112-19
Sequence 19, Application US/08478312
Sequence 19, Application US/08478312
Sequence 19, Application US/08478312
Sequence 19, Application US/08478312
Sequence 19, Application US/084710N:
APPLICANT: Barrett. Ronald W.
APPLICANT: Scharz Peter
APPLICANT: Sloan, Derek
APPLICANT: Sloan, Min-Jia
TITLE OF INVENTION: Receptor
ITILE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESSS:
APPLICANT: All Miranda Ave.
STREET: 4001 Miranda Ave.
CUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Gaps
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Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,312
FILING DATE: 07-JUN-1995
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0
  Mismatches
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Patent No. 5668110
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 1088
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Barrett, Ronald W. APPLICANT: England, Bruce APPLICANT: Schatz, Peter APPLICANT: Sloan, Derek APPLICANT: Chen, Min-Jia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
  10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: peptide US-08-478-312-19
                                          1 CXXXXXXX 10
                                                                               3 CXXXXXXXX 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-485-302-19
  Matches
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                                                                                                                                                                                                                           ; Score 26; DB 4; Length 28;
; Pred. No. 10;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEPTIDES AND METHODS OF ND USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/S00,124
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 36, Application US/09500124

Patent No. 643220

GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: OULLIAM, Lawrence A.
APPLICANT: PER, Chaming J.
APPLICANT: FOWLES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AN TITLE OF INVENTION: 1SOLATING AND USING SAM NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & man-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STARE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMABR:
PILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENE/DOCKET NUMBER: 1101-20;
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (212) 790-9090
TELEFRAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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INFORMATION FOR SEQ ID NO: 36:
  (703) 413-3000
               TELEFAX: (703) 413-220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                         TOPOLOGY: unknown; MOLECULE TYPE: protein US-08-278-865-36
                                                                                                                                                                                                                                                                                                             1 CXXXXXXXC 10
                                                                                                                                                                                                                                                                                                                                                   CXXXXXXXX 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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Best Local Similarity
                                                                                                                         amino acid
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: U.S.A.
  TELEPHONE:
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RESULT 34
US-08-484-083-15
is Gauence 15, Application US/08484083
is Patent No. 5683983
is Garrett, Ronald W.
APPLICANT: Barrett, Ronald W.
APPLICANT: Gohatz, Peeter
APPLICANT: Gohatz, Peeter
APPLICANT: Chen, Min-Jia
TITLE OF INVENTION: Peptides and Compounds That Bind to the IL-5
TITLE OF INVENTION: Receptor
NUMBER OF SCHENCES: 65
CORRESPONDENCES: 65
CORRESPONDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 26, DB 1, Length 31, Pred. No. 11, 0, Mismatches 0; Indels
                                    1088.2A
                             REFERENCE/DOCKET NUMBER: 108E
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-496-230
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
      REGISTRATION NUMBER: 36,691
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%;
Matches 10; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
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                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: peptide US-08-476-169-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CXXXXXXXX 10
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                                                                                                                                                                                                                       LENGTH: 31 amino TYPE: amino acid STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                    linear
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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Patent No. 5677280
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Schatz, Peter
APPLICANT: Schatz, Peter
APPLICANT: Chen, Min-Jia
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, N.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 26; DB 1; Length 31; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: ENDER Compatible
COMPUTER: ENDER COMPUTER: ENDER COMPUTER: ENDER COMPUTER: ENDER COMPUTER: DEFENTING SYSTEM: PC-DOS/MS-DOS
COMFUTENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,302
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36.691
REFERENCE/DOCKET NUMBER: 1088.1B
TELECOMMUNICATION INFORMATION:
TELEFONE: 415-496-2300
TELEFONE: 415-496-2300
TELEFONE: 415-496-2300
TELEFONE: A15-496-2300
TELEFONE: A15-496-2300
TELEFONE: A15-406-2300
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,169
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
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NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSED: Affymax Technologies, N.V.
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Affymax Technologies, N.V. 4001 Miranda Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%;
Matches 10; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide US-08-485-302-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CXXXXXXXC 10
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CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 33
US-08-476-169-15
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APPLICANT: DeRose, Richard
APPLICANT: Freyssinet, Georges
APPLICANT: Freyssinet, Georges
APPLICANT: Hoffman, Unles
TITLE OF INVENTION: Chimeric Gene Encoding Drosomycin,
TITLE OF INVENTION: Vector Containing It And Production of Disease-Resistant
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: A3289-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/480,251
CURRENT FILING DATE: 2000-01-11
PRIOR FILING DATE: 1998-07-08
PRIOR FILING DATE: 1998-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Modified-site
LOCATION: 14
OTHER INFORMATION: /note= "Xaa, if present, is any amino acid"
FEATURE: Modified-site
LOCATION: 16-25
OTHER INFORMATION: /note= "Xaa is any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KSY: Modified-site
LOCATION: 26, 27, 28
OTHER INFORMATION: /note= "Xaa, if present, is any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
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100.0%; Score 26; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 10; Conservative 0; Mismatches 0; Indels
FILING DATE: 8-SEP-1995
CLASSIFICATION: 5:30
ATTORNEY/AGENT INFORMATION:
NAME: KAZEA, Catherine J.
NEGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: 41,106
TELEPAN: (617) 242-7400
TELEPAN: (617) 742-4214
INFORMATION FOR SEQ ID NO: 7:
SEQUENCY: (617) 742-4214
INFORMATION acids
TYPE: amino acid
TYPE: amino acid
TYPE: mino acid
TYPE: mino acid
TYPE: Modified-site
NOLECULE TYPE: Internal
FRAGMENT TYPE: Internal
RAME/KEY: Modified-site
LOCATION: 2-8
OTHER INFORMATION: /note= "Xaa is any amino acid"
FRATURE:
NAME/KEY: Modified-site
LOCATION: 10-13
OTHER INFORMATION: /note= "Xaa is any amino acid"
FRATURE:
NAME/KEY: MODIfied-site
LOCATION: 10-13
OTHER INFORMATION: /note= "Xaa is any amino acid"
FRATURE:
FRA
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LOCATION: 32-39

COTHER INFORMATION: /note= "Xaa is any amino acid"

US-08-525-864A-7
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LOCATION: 30
OTHER INFORMATION: /note= "Xaa is any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-480-251-15
; Sequence 15. Application US/09480251
Patent No. 6465719
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 CXXXXXXXC 40
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                                                                                                                                                                                                                                                                                                                                   GENERAL INCRAMINATION:
GENERAL INCREMATION:
GENERAL INCREMATION:
APPLICANT: STEM CELL PHARMACEUTICALS, INC.
APPLICANT: TWARDZIK, Daniel R.
APPLICANT: PERNET, Andre
APPLICANT: PERKER, Thomas S.
APPLICANT: SOO-08-17
PRIOR APPLICATION NUMBER: US 09/459, 813
PRIOR APPLICATION NUMBER: US 09/459, 813
PRIOR APPLICATION NUMBER: US 09/459, 813
PRIOR APPLICATION NUMBER: US 09/459, 935
PRIOR FILING DATE: 1999-12-13
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 8
AND APPLICATION NUMBER: US 09/378, 567
AND APPLICATION NUMBER: US 09/378, 567
APPLICANT: PERKER: PARENTIN VERSION 3.1
SEQ ID NO 8
AND APPLICATION NUMBER: US 09/378, 567
AND APPLICATION NUMBER: US 09/378, 567
APPLICANT: PERKER: PARENTIN VERSION 3.1
SEQ ID NO 8
AND APPLICATION NUMBER: US 09/378, 567
AND APPLICATION NU
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US-08-25-864A-7
IS Sequence 7, Application US/08525864A
Fatent No. 5912326
Fatent No. 5912326
GARBEAL INFORMATION:
APPLICANT: Chang, Han
TITLE OF INVENTION: Related thereto
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS;
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 26; DB 4; Length 36; 100.0%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 28 STREET
STREET: 28 STREET
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/525,864A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1). 7(36); OTHER INFORMATION: Xaa is any amino acid
US-10-138-158-8
                                                                                                                                                                                                                                                                                             Sequence 8, Application US/10138158
Patent No. 6677307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CXXXXXXXX 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: MISC FEATURE LOCATION: (1)..(36)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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FEATURE:
NAME/KEY: VARIANT
NAME/KEY: VARIANT
(6) . . . (6)
OTHER INFORMATION: Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, Tyr
OTHER INFORMATION: or Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
NAME (11)...(11)
OTHER INFORMATION: Xaa is any residue except Ala, Cys, Glu, His, Ile,
OTHER INFORMATION: Pro, Trp and Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (7)...(7)
OTHER INFORMATION: Xaa is any residue except Asn, Cys, Gly, His, Leu,
OTHER INFORMATION: Met, Phe or Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: VARIANT
LOCATION: (2) ... (2) ... (3) OCHER INFORMATION: Xaa is any residue except Asp, Cys, Gly, His, Met, OTHER INFORMATION: Pro, Trp or Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOME, KEY: VARIANT
LOCATION: (5)...(5)
OTHER INFORMATION: Kaa is any residue except Asn, Cys, Gln, Gly, Phe,
OTHER INFORMATION: Ser, Thr or Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         residue except Arg, Cys, Met, Phe, Trp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: VARIANT
LOCATION: (9)...(9)
OTHER INFORMATION: Xaa is Pro, Arg, Leu, Val, Ser, Asp, Ile, Asn or
OTHER INFORMATION: Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: VARIANT
LOCATION: (3)...(3)
OTHER INFORMATION: Xaa is Leu, Glu, Met, Gln, Phe, Ser, Thr, Ala or
OTHER INFORMATION: Pro
                                                                                                                 RESULT 38
US-095-15
US-095-17
US-095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (8)...(8)
OTHER INFORMATION: Xaa is Gly or Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: polypeptide motif FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             any
Val
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAMEKEY: VARIANT
LOCATION: (4)
OTHER INFORMATION: Xaa is ar
OTHER INFORMATION: Tyr or Ve
       1 CXXXXXXXX 10
                                                 CXXXXXXXXX 11
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NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                            용
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Best Local Similarity 100.0%; Pred. No. 12;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ION: (25)...(31)
INFORMATION: Preferably Glu Glu Gly Arg Ser Ser Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (4)...(9)
OTHER INFORMATION: Preferably Ser Gly Arg Tyr Lys Gly
NAME-KEY: VARIANT
LOCATION: (13)...(17)
OTHER INFORMATION: Preferably Val Trp Asp Asn Glu
                                                                                                                                                                                                                                                                  FEATURE:
OTHER INFORMATION: Drosomycin core sequence
NAME/KEY: VARIANT
LOCATION: (1)...(1)
OTHER INFORMATION: Perferably Asp
NAME/KEY: VARIANT
LOCATION: (3)...(3)
OTHER INFORMATION: Preferably Leu
NAME/KEY: VARIANT
PRIOR APPLICATION NUMBER: FRANCE 9709,663
PRIOR FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 15
LENGTHARE: FastSEQ for Windows Version 3.0
SEQ ID NO 15
LENGTH: 44
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (35)...(37)
OTHER INFORMATION: Preferably Pro Ser Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (38)...(38)
OTHER INFORMATION: Preferably Lys
NAME/KEX: VARIANT
LOCATION: (40)
OTHER INFORMATION: Preferably Trp
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (42)...(42)
OTHER INFORMATION: Preferably Glu
NAME/KEY: VARIANT
COTATION: (43)...(43)
OTHER INFORMATION: Preferably Gly
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (34)...(34)
OTHER INFORMATION: Preferably Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAMERA EM. NAMERANT
NAMER INCOMMATION: (22)
OTHER INFORMATION: Preferably Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ION: (21)...(21)
INFORMATION: Preferably Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (10) ... (10)
OTHER INFORMATION: Preferably Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (12)...(12)
OTHER INFORMATION: Preferably Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME, KEY: VARIANT
LOCATION: (18)...(18)
OTHER INFORMATION: Preferably Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (20)...(20)
OTHER INFORMATION: Preferably Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OCATION: (32)...(32)
THER INFORMATION: Preferably His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: VARIANT
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or Pro
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                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (35)...(35)
OTHER INFORMATION: Xaa is Gly, Lys, Arg, Pro, Gln, Leu, Glu, Asn or Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KRY: VARIANT
LOCATION: (42)...(42)
OTHER INFORMATION: Xaa is any residue except Cys, Gln, Gly, Phe or Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: VARIANT
LOCATION: (45)...(45)
OTHER INFORMATION: Xaa is Glu, Asp, Ala, His, Met, Val, Gln, Lys, Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is any residue except Cys, His, Ile, Phe, Pro,
Thr, Trp, Tyr or Val
                                 LOCATION: (30)...(30)
OTHER INFORMATION: Xaa is any residue except Arg, Cys, Gly or Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
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Best Local Similarity 100.0%; Pred. No. 13;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FERTURE:
LOCATION: (40)...(40)
OTHER INFORMATION: Xaa is Arg, Asn, Lys, Gln or Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEATURE:
OAM:/KEY: VARIANT
LOCATION: (43)...(43)
OTHER INFORMATION: Xaa is Thr, Ser, Arg, Lys or Asp
                                                                                                                                           Phe or Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: VARIANT
LOCATION: (41)...(41)
OTHER INFORMATION: Xaa is Phe, Tyr or Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (36) ... (36) DTHER INFORMATION: Xaa is Gly, Lys or Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (37)...(37)
OTHER INFORMATION: Xaa is Asn, Lys or Ser
                                                                                                                                                                                                           LOCATION: (32)...(32)
OTHER INFORMATION: Xaa is Ser, Gly or Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: VARIANT
LOCATION: (39)...(39)
OTHER INFORMATION: Xaa is Asn or Tyr
                                                                                                                                                                                                                                                                                                  LOCATION: (33)...(33)
OTHER INFORMATION: Xaa is Gly or Ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leu,
                                                                                                                                           is Tyr, Trp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: VARIANT
LOCATION: (44) ... (44)
OTHER INFORMATION: Xaa is Ile,
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CXXXXXXXXX 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (38)...(38)
OTHER INFORMATION: Xaa
OTHER INFORMATION: T
                                                                                              NAME/KEY: VARIANT
LOCATION: (31)...(31)
OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (37)
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                                                                                                                                                                   FEATURE:
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                    IAME/KEY: VARIANT
                                                                                                                                                                                                                                                                               IAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: VARIANT
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US-09-523-487-5
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THER INFORMATION: Xaa is any residue except Asp, Cys, His, Ile, Phe, Trp or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: VARIANT
LOCATION: (28)...(28)
OTHER INFORMATION: Xaa is any residue except Asn, Asp, Cys, His, Ile, Pro, Trp,
OTHER INFORMATION: Tyr or Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tyr or Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (27)...(27)
OTHER INFORMATION: Xaa is any residue except Cys, Gly, Phe, Pro, Ser or Trp
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMME/KEY: VARIANT
JOCATION: (21)...(21)
DTHER INFORMATION: Xaa is any residue except Asp, Cys, Glu, His or Tyr
NAME/KEY: VARIANT
LOCKTION: (12)...(12)
OCHER INFORMATION: Xaa is Arg, Lys, Ala, Asp, Gln, Phe, Gly, Glu, Thr
OTHER INFORMATION: and Ser
                                                                                                                                                                                                                      NAME/KEY: VARIANT
LOCATION: (14)...(14)
OTHER INFORMATION: Xaa is any residue except Arg, Asn, Cys, Gly, His,
OTHER INFORMATION: Ser, Trp or Tyr
                                                                                                                                                                                                                                                                                                                                                    CCATION: (15)...(15)
DIHER INFORMATION: Xaa is any residue except Ala, Asp, Cys, Gly, His,
DIHER INFORMATION: Met, Trp or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                     OCATION: (16)...(16)
THER INFORMATION: Xaa is Ser, Ala, Arg, Val, Gln, Lys, Leu, Gly or THER INFORMATION: 11e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ile, Gln, Glu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OCCATION: (22)...(22)
THER INFORMATION: Xaa is any residue except Cys, Met, Pro or Trp
                                                                                       LUCATION: (13)...(13)
OTHER INFORMATION: Xaa is any residue except Asp, Cys, Glu, Pro, OTHER INFORMATION: or Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'EATURE:
AANETON: (24)...(24)
OTHER INFORMATION: Xaa is Lys, Gln, Asn, His, Gly, Arg or Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OCATION: (18)...(18)
THER INFORMATION: Xaa is Tyr, His, Phe, Trp, Asn or Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trp or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ser or Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OCATION: (23)...(23)
THER INFORMATION: Xaa is Ala, Lys, Ser, Leu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: VARIANT
LOCATION: (29)...(29)
OTHER INFORMATION: Xaa is Phe or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       )CATION: (19)...(19)
THER INFORMATION: Xaa is Tyr or Phe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tyr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OCATION: (20)...(20)
THER INFORMATION: Xaa is Lys, Asn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is Phe,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATION: (17)...(17)
HER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SATURE:
AME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: VARIANT
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                                                                                     FEATURE:
NAME/KEY: VARIANT
LOCATION: (13)...(
                                                                                                                                                                                                                                                                                                                'EATURE:
TAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                           'EATURE:
IAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AME/KEY: VARIANT
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NAME/KEY: VARIANT
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OTHER INFORMATION: Xaa is any residue except Asn, Cys, Gly, His, Leu, OTHER INFORMATION: Met, Phe or Trp
NAME/KEY: VARIANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAME/KEY: VARIANT
LOCATION: (11)
OTHER INFORMATION: Xaa is any residue except Ala, Cys, Glu, His, Ile,
OTHER INFORMATION: Ro, Trp and Val
NAME/KEY: VARIANT
LOCATION: (12):...(12)
OTHER INFORMATION: Xaa is Arg, Lys, Ala, Asp, Gln, Phe, Gly, Glu, Thr
OTHER INFORMATION: and Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOCATION: (15)...(15)
OTHER INPORMATION: Xaa is any residue except Ala, Asp, Cys, Gly, His, OTHER INFORMATION: Met, Trp or Tyr
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Xaa is any residue except Arg, Cys, Met, Phe, Trp, OTHER INFORMATION: Tyr or Val
NAME/KEY: VARIATION: Tyr or Val
NAME/KEY: VARIATION: Tyr or Val
OTHER INFORMATION: Xaa is any residue except Asn, Cys, Gln, Gly, Phe, OTHER INFORMATION: Ser, Thr or Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAMBIKEY: VARIANT
LOCATION: (13)...(13)
OTHER INFORMATION: Xaa is any residue except Asp, Cys, Glu, Pro, Thr
OTHER INFORMATION: Or Trp
NAMB/KEY: VARIANT
LOCATION: (14)...(14)
OTHER INFORMATION: Xaa is any residue except Arg, Asn, Cys, Gly, His
OTHER INFORMATION: Ser, Trp or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DUCATION: (2)...(2)
OTHER INFORMATION: Xaa is any residue except Asp, Cys, Gly, His, Met,
NAMER INFORMATION: Pro, Trp or Val
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: VARIANT
LOCATION: (8)...(8)
OTHER INFORMATION: Xaa is Gly or Glu
MAME/KEY: VARIANY
LOCATION: (9)...(9)
OTHER INFORMATION: Xaa is Pro, Arg, Leu, Val, Ser, Asp, Ile, Asn or
OTHER INFORMATION: Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phe, Ser, Thr, Ala or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT
LOCATION: (6)...(6)
COTHER INFORMATION: Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser,
OTHER INFORMATION: or Met
NAME/KEY: VARIANT
                                  GENERAL INFORMATION:
APPLICANT: Conklin, Darrell C.
APPLICANT: Foster, Donald C.
APPLICANT: Foster, Donald C.
APPLICANT: Foster, Donald C.
APPLICANT: Foster, Donald C.
APPLICANT: Geren
TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE AND MATERIALS
TITLE OF INVENTION: AND METHODS FOR MAKING IT
FILE REPERENCE: 98-22
CURRENT APPLICATION NUMBER: US/09/523,487
CURRENT APPLICATION NUMBER: 09/320,095
PRIOR FILING DATE: 1999-05-66
NUMBER OF SEQ ID NOS: 20
SEQ ID NO 5: SEQ ID NO 5: 20
IENGTH: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (3)...(3)
DTHER INFORMATION: Xaa is Leu, Glu, Met, Gln, OTHER INFORMATION: Pro
AMES/KEY: VARANT
LOCATION: (4)...(4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: polypeptide motif
NAME/KEY: VARIANT
Sequence 5, Application US/09523487
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OTHER INTORMATION: As a is Ser, Ala, Arg, Val, Gln, Lys, Leu, Gly OT
COTHER INTORMATION: As a is Ser, Ala, Arg, Val, Gln, Lys, Leu, Gly OT
COTHER INTORMATION: As a is The Try IIIe, Try or Leu
COCATION: (10)...(10)
COCATION: (10)...(10)
COCATION: (10)...(10)
COCATION: (20)...(20)
COCATION: (20)...(20)
COCATION: (20)...(20)
COCATION: (20)...(20)
COCATION: (20)...(20)
COCATION: (20)...(21)
COCATION: (20)...(21)
COCATION: (20)...(21)
COCATION: (20)...(22)
COCATION: (20)...(23)
COCATION: (20)...(24)
COCATI
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NAME/KEY: VARIANT
LOCATION: (14)...(14)
OTHER INFORMATION: Xaa is any residue except Arg, Asn, Cys, Gly, His, Ser, Trp
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OTHER INFORMATION: Xaa is Ala, LyB, Ser, Leu, Thr, Ile, Gln, Glu, Tyr or Val
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gly, His, Met,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (15)...(15)
OTHER INFORMATION: Xaa is any residue except Ala, Asp, Cys, Gly, His, Me OTHER INFORMATION:
FEBRUNE:
FORMATION: (16)...(16)
OTHER INFORMATION: Xaa is Ser, Ala, Arg, Val, Gln, Lys, Leu, Gly or Ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: VARIANT
LOCATION: (21)...(21)
DTHER INFORMATION: Xaa is any residue except Asp, Cys, Glu, His or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cys, Glu, Pro or Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: VARIANT
LOCATION: (12) ... (12)
THER INFORMATION: Xaa is Arg, Lys, Ala, Asp, Gln, Phe, Gly, Glu, Thr
DTHER INFORMATION: or Ser
NAME/KEY: VARIANT
LOCATION: (6)...(6)
OTHER INFORMATION: Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, Tyr
OTHER INFORMATION: or Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT 11)
LOCHTON: (11)...(11)
OCHER INFORMATION: Xaa is any residue except Ala, Cys, Glu, His, Ile, OTHER INFORMATION: Yao, Trp or Val
                                                                                                  FEATURE:
NAME/KEY: VARIANT
NAME/KEY: (7)...(7)
OTHER INFORMATION: Kaa is any residue except Asn, Cys, Gly, His, Leu,
OTHER INFORMATION: Met, Phe or Trp
                                                                                                                                                                                                                                                                                                                                                                                           Val, Ser, Asp, Ile, Asn or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/CATION: (22)...(22)
OTHER INFORMATION: Xaa is any residue except Cys, Met, Pro or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: VARIANT
LOCATION: (18)...(18)
OTHER INFORMATION: Xaa is Tyr, His, Phe, Trp, Asn or Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COCATION: (13)...(13)

THER INFORMATION: Xaa is any residue except Asp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trp or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tyr, Ile,
                                                                                                                                                                                                                                                                                                                                                                                              is Pro, Arg, Leu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (20)....(20)
DIHER INFORMATION: Xaa is Lys, Asn, Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (19)...(19)

THER INFORMATION: Xaa is Tyr or Phe
                                                                                                                                                                                                                                                                         LOCATION: (8)...(8)
OTHER INFORMATION: Xaa is Gly or Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEX: VARIANT
LOCATION: (17)...(17)
OTHER INFORMATION: Xaa is Phe,
                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: VARIANT
LOCATION: (9)...(9)
OTHER INFORMATION: Xaa ii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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NAME/KEY: VARIANT
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                                                                                                                                                                                                                                                 NAME/KEY: VARIANT LOCATION: (8)...(
                                                                                                                                                                                                                                                                                            CTHER INFORMATION: Xaa is Glu, Lys, Gln, Asp, Ala or Tyr
NAME/KEY: VARIANT
INCATION: (48)...(48)
OTHER INFORMATION: Xaa is any residue except Ala, Cys, Gly, Phe, Pro, Ser, Thr, Trp
NAME/KEY: VARIANT
NAME/KEY: VARIANT
OTHER INFORMATION: (49)...(49)
OTHER INFORMATION: Xaa is any residue except Cys, Ile, Leu, Met, Phe, Pro, Ser, Tyr
NAME/KEY: VARIANT
OTHER INFORMATION: (50)...(50)
COTHER INFORMATION: Xaa is Thr, Ala, Val, Ile, Phe, Leu, Met, Lys, Tyr or Arg
                                                                                                                                                                                                         NAME/KEY: VARIANT
LOCATION: (45)...(45)
OTHER INFORMATION: Xaa is Glu, Asp, Ala, His, Met, Val, Gln, Lys, Arg or Pro
                                                                                                                                                                                 Leu, Trp, Arg, Lys, Thr, Glu, Ala, Gln or Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
             LOCATION: (42)...(42)
OTHER INFORMATION: Xaa is any residue except Cys, Gln, Gly, Phe or Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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LOCATION: (5)...(5)
OTHER INFORMATION: Xaa is any residue except Asn, Cys, Gln, Gly, Phe,
OTHER INFORMATION: Ser, Thr or Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phe, Trp
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NAME/KEY: VARIANT
LOCATION: (3) -1. (3)
OTHER INFORMATION: Xaa is Leu, Glu, Met, Gln, Phe, Ser, Thr, Ala
OTHER INFORMATION: Pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

100.0%; Score 26; DB 3; Length 51;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         residue except Asp, Cys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3. Application US/09388183
Sequence 3. Application US/09388183
Setent No. 6380354
GENERAL INFORMATION:
APPLICANT: CONCLIN, Darrell C.
TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE ZKUN6
FILE REPERENCE: 98-40
CURRENT APPLICATION NUMBER: US/09/388,183
CURRENT FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 7
SOCTHARAR: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 51
                                                                               LOCATION: (43)...(43)
OTHER INFORMATION: Xaa is Thr, Ser, Arg, Lys or Asp
NAME/KEY PARIANT
LOCATION: (44)...(44)...
OTHER INFORMATION: Xaa is 11e, Leu, Trp, Arg, Lys, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Pro
FEATURE:
LOCATION: (4)...(4)
OTHER INFORMATION: Xaa is any residue except Arg,
OTHER INFORMATION: Tyr or Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
OTHER INFORMATION: Kunitz motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: VARIANT
LOCATION: 0...(2)
OTHER INFORMATION: Xaa is any
OTHER INFORMATION: Pro or Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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                                                             NAME/KEY: VARIANT
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US-09-388-183-3
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NAME/KEY: VARIANT
LOCATION: (48)...(48)
OTHER INFORMATION: Xaa is any residue except Ala, Cys, Gly, Phe, Pro, Ser, Thr,
                                                                                     LOCATION: (45)...(45)
OTHER INFORMATION: Xaa is Glu, Asp, Ala, His, Met, Val, Gln, Lys, Arg or Pro
FEATURE:
LOCATION: (44)...(44)
OTHER INFORMATION: Xaa is Ile, Leu, Trp, Arg, Lys, Thr, Glu, Ala, Gln or Val
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US-08-525-864A-8
US-08-525-864A-8
Sequence 8, Application US/08525864A
Facent NO. 5912126
GENERAL INFORMATION:
APPLICANT: Chang, Han
ITILE OF INVENTION: Related thereto
ITILE OF INVENTION: Related thereto
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 28 State Street
CITY: Boston
CITY: Boston
CITY: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                             LOCATION: (46)...(46)
OTHER INFORMATION: Xaa is Glu, Lys, Gln, Asp, Ala, Tyr or Ser
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 41
US-09-740-510-5
Sequence 5, Application US/09740510
Sequence 6, Application US/09740510
FRENCE INFORMATION:
APPLICANT: HOLDOWAY, James L.
TITLE OF INTENTION:
CURRENT APPLICATION KUNITZ Domain Polypeptide Zkunl1
FILE REFERENCE: 99-103
CURRENT APPLICATION NUMBER: US/09/740,510
CURRENT FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASTENCE for Windows Version 3.0
SEQ ID NO 5
LENGTH: SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 26; DB 4;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 10; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: motif.
; NAME/KEY: VARIANT
; LOCATION: (1)...(51)
; OTHER INFORMATION: Xaa is any amino acid.
US-09-740-510-5
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXXXXXXXXX 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXXXXXXXX 10
                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: VARIANT
LOCATION: (49)
                                             FEATURE:
NAME/KEY: VARIANT
                                                                                                                                                        NAME/KEY: VARIANT
                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAME/KEY: VARIANT
JOCATION: (38)...(38)
OTHER INFORMATION: Xaa is any residue except Cys, His, Ile, Phe, Pro, Thr, Trp, Tyr
                                                                                                                                  is any residue except Asn, Asp, Cys, His, Ile, Pro, Trp, Tyr
                                                                                                                                                                                                                                                                                             OCATION: (28)...(28)
OTHER INFORMATION: Xaa is any residue except Asp, Cys, His, Ile, Phe, Trp or Tyr
                                                                                                                                                                                                        LOCATION: (27)...(27)
OTHER INFORMATION: Xaa is any residue except Cys, Gly, Phe, Pro, Ser or Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ION: (35)...(35) INFORMATION: Xaa is Gly, Lys, Arg, Pro, Gln, Leu, Glu, Asn or Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: VARIANT
LOCATION: (42)...(42)
OTHER INFORMATION: Xaa is any residue except Cys, Gln, Gly, Phe or Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AME/KEY: VARIANT
OCATION: (30)...(30)
THER INFORMATION: Xaa is any residue except Arg, Cys, Gly or Met
         LOCATION: (24)...(24)
OTHER INFORMATION: Xaa is Lys, Gln, Asn, His, Gly, Arg or Met
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: VARIANT
LOCATION: (43)...(43)
UNIER INFORMATION: Xaa is Thr, Ser, Arg, Lys or Asp
PERTURE: NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OCATION: (40)...(40)
THER INFORMATION: Xaa is Arg, Asn, Lys, Gln or Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "EATURE:
NAME/KEY: VARIANT
NOCATION: (41)...(41)
THER INFORMATION: Xaa is Phe, Tyr or Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NWE/KEY: VARIANT
OCATION: (36)...(36)
THER INFORMATION: Xaa is Gly, Lys or Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OCATION: (37) ... (37)
THER INFORMATION: Xaa is Asn, Lys or Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OCATION: (33)...(33)
THER INFORMATION: Xaa is Gly or Ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ION: (39)...(39)
INFORMATION: Xaa is Asn or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                           is Phe or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OCATION: (31)...(31)
THER INFORMATION: Xaa is Tyr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is Ser,
                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: VARIANT
COCATION: (29)
THER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OCATION: (32)...(32)
THER INFORMATION: Xaa
                                                                                                               LOCATION: (25)...(25)
OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EATURE:
AME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AME/KEY: VARIANT OCCATION: (39)...
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                                                                                            NAME/KEY: VARIANT
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                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT
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Application US/08667025
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LOCATION: 30, 31, 32, 33, 34, 35, 36, 37, 38,39
OTHER INFORMATION: /note= "Xaa, if present, is any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAWE/KEY: Modified-site

LOCATION: 51, 52, 53, 54, 55, 56

COTHER INFORMATION: /note= "Xaa, if present, is any amino acid"

12-08-525-864A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Modified-site
LOCATION: 6, 7, 8, 9, 10, 11, 12, 13, 14, 15
OTHER INFORMATION: /note= "Xaa, if present, is any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEX: Modified-site
LOCATION: 20, 21, 22, 23, 24
OTHER INFORMATION: /note= "Xaa, if present, is any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 26; DB 2; Length 57; 100.0%; Pred. No. 14; tive 0; Mismatches 0; Indels
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LOCATION: 26-29
OTHER INFORMATION: /note= "Xaa is any amino acid"
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LOCATION: 43-50
OTHER INFORMATION: /note= "Xaa is any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 2-5
OTHER INFORMATION: /note= "Xaa is any amino acid"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 17-19
OTHER INFORMATION: /note= "Xaa is any amino acid"
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OTHER INFORMATION: /note= "Xaa is any amino acid'
                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,864A
FILING DATE: B-SEP-1995
CLASSIFICATION: 530
ATTORNEY/ACENT INFORMATION:
REGISTRATION NUMBER: 41,106
REGISTRATION NUMBER: HUI-017
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATI
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NAME/KEY: Modified-site
                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Modified-site
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGWENT TYPE: internal
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CXXXXXXXC 10
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RESULT 43

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RESULT 44
US-08-475-174-1

| Sequence 1, Application US/08475174
| Sequence 1, Application US/08475174
| Sequence 1, Application US/08475174
| Parent No. 5932622
| GENERAL INFORMATION:
| APPLICANT: Boolm, Marcus F. APPLICANT: Heyman, Richard A. APPLICANT: Boolm, Marcus F. APPLICANT: Heyman, Richard A. APPLICANT: Heyman, Richard A. APPLICANT: Holor, Christina FITLE OF INVENTION: MEDANS FOR THE MODULATION OF PROCESSES FITLE OF INVENTION: MEDANS FOR THE MODULATION OF PROCESSES FITLE OF INVENTION: MEDANS FOR THE MODULATION OF PROCESSES ITLE OF INVENTION: MEDANS FOR THE MODULATION OF PROCESSES ITLE OF INVENTION: MEDANS FOR THE MODULATION OF PROCESSES ITLE OF INVENTION: MEDANS FOR THE MODULATION OF PROCESSES ITLE OF INVENTION: MEDANS FOR THE MODULATION OF PROCESSES ITLES OF INVENTION: MEDANS FOR THE MODULATION OF PROCESSES ITLES OF INVENTION: MEDANS FOR THE MODULATION OF PROCESSES ITLES OF INVENTION: MEDANS FOR THE MODULATION OF PROCESSES ITLES OF INVENTION: MEDANS FOR THE MODULATION OF PROCESSES ITLES OF INVENTION: MEDANS FOR THE MODULATION OF PROCESSES ITLES OF INVENTION: MEDANS FOR THE MODULATION OF PROCESSES ITLES OF INVENTION: MEDANS FOR THE MODULATION OF PROCESSES ITLES OF INVENTION: MEDANS FOR THE MODULATION OF PROCESSES ITLES OF INVENTION: MEDANS FOR THE MODULATION OF PROCESSES ITLES OF INVENTION OF PROCESSES ITLES OF INVENTION OF IN
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                                                                                                                                                                                                                                                                                                                                            CONTEXT ADDRESSED.

STREET: 4365 Executive Drive, Suite 1600
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92121-2189
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/67,025
FILING DATE:
FLING DATE:
REGISTRATION INFORMATION:
NAME: Rames, ROBERT T.
REGISTRATION INFORMATION:
NAME: RAMES RAMES ROBERT TO TELEFRATION INFORMATION:
TELEFRATION NUMBER: 37,915
REFINENCE/DOCKET NUMBER: 97,915
TELEFRATION NUMBER: 137,915
TELEFRATION NUMBER: 1477
TELEFRATION NUMBER: 17,915
TELEFRATION NUMBER: 17,915
TELEFRATION NUMBER: 17,915
TELEFRATION NUMBER: 17,915
GENERAL INPORMATION:
APPLICANT: Gage, Frederick H.
APPLICANT: Suhr, Steven T.
TITLE OF INVENTION: WECTORS AND
TITLE OF INVENTION: UECTORS AND
TITLE OF INVENTION: UES THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 26; DB 2;
; Pred. No. 15;
0; Mismatches 0
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Best Local Similarity 100.0%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 71 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 619-677-1477
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: not relevan
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CXXXXXXXX 10
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US-00-3/C-10-1

Sequence 1, Application US/08372218

Patent No. 5990163

GENERAL INFORMATION:
APPLICANT: Bayman, Ronald M.
APPLICANT: Harmon, Margaret A.
APPLICANT: Boehm, Margaret A.
APPLICANT: Boehm, Margaret A.
APPLICANT: Harmon, Margaret A.
APPLICANT: Harmon, Margaret A.
APPLICANT: Harmon, Margaret A.
APPLICANT: Boehm, Wargaret A.
APPLICANT: Harmon, Margaret A.
APPLICANT: Boehm, Wargaret A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
OTHER INFORMATION: Nuclear/intracellular receptors
FEATURE:
NAME/KEY: VARIANT
OTHER INFORMATION: Residues that are almost universally conserved,
OTHER INFORMATION: Residues that are almost universally conserved,
OTHER INFORMATION: Dut for which variations have been found in some
FEATURE:
NAME/KEY: VARIANT
IOCATION: (1)...(71)
OTHER INFORMATION: Xaa = No. 5990163-conserved Amino Acids within the
US-08-372-218-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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100.0%; Score 26; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 10; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 15; Length 71;
Matches 10; Conservative 0; Mismatches 0; Indels
             ATTING DATE: 18-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION UNDERE: US 07/809,980
FILING DATE: 18-DEC-1991
ATTORNEY/AGENT INFORWATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9979
TELEPHONE: 619-646-1995
TELEPAX: 619-546-1995
TELEFAX: 619-546-1995
TELEFAX: 619-546-1995
TELEFAX: 619-546-1995
TELEFAX: 71 anino acid
ENDIN: 71 anino acid
WO 93/11755
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acids TOPOLOGY: "Interest and acids TOPOLOGY: "Interest and acids TOPOLOGY: "Interest and acids TOPOLOGY: "Interest and acids 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CXXXXXXXX 10
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US-08-372-218-1
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Patent No. 596899
GENERAL INFORMATION:
PAPLICANT: Evans, Ronald M.
PPELICANT: Hampelsdorf, David J.
PAPLICANT: Hampelsdorf, David J.
PAPLICANT: Hampelsdorf, David J.
PAPLICANT: Boohm, Marcus F.
APPLICANT: Bichele, Gregor
APPLICANT: Bichele, Gregor
ITILE OF INVENTION: MEDIATED BY RETINOID RECEPTORS AND COMPOUNDS USEFUL
ITILE OF INVENTION: THEREFOR
INTILE OF INVENTION: THEREFOR
INTILE OF INVENTION: THEREFOR
INTILE OF INVENTION: ADDIATED BY RETINOID RECEPTORS AND COMPOUNDS USEFUL
ITILE OF INVENTION: THEREFOR
INTILE OF INVE
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100.0%; Score 26; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 10; Conservative 0; Mismatches 0; Indels
                                         COMPUTER: READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ENDER Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SUSTANER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,174
FILING DATE:
CLASSITICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: US/08/980
FILING DATE: 1991-12-18
ATTORNEY/AGENT INFORMATION:
AMME: Reiter Seephen E.
REGISTATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: 931,192
REFERENCE/DOCKET NUMBER: 931,192
REFERENCE/DOCKET NUMBER: 931,192
REFERENCE/DOCKET NUMBER: 931,193
REFERENCE/DOCKET NUMBER: 931,193
REFERENCE/DOCKET NUMBER: 931
TELEPHAN: (619) 546-9392
INFORMATION EN SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
MANDE: APPLICATION OCCUPANTION FOR PARIOR PARIOR FOR PARIOR F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: BAR PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995
07-JUN-1995
07-JUN-1995
07-JUN-1995
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CLASSIFICATION: 424
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,857
FILING DATE: 14-JUN-1994
PRICR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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Sequence 3, Application US/08486403
Patent No. 6281330
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Best Local Similarity 100.0%;
Matches 10; Conservative
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CLASSIFICATION: 435
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STREET: 444 South F
CITY: Los Angeles
STATE: California
COUNTRY: United Sta
ZIP: 90071
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US-08-486-403-3
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                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: EVANS, RONALD M.
APPLICANT: EVANS, RONALD M.
APPLICANT: MCKEOWN, MICHAEL B.
APPLICANT: MCKEOWN, MICHAEL B.
APPLICANT: SEGRAVES, WILLIAM A.
APPLICANT: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: RECEPTOR-DEFICIENT ANIMALS AND CELL LINES DERIVED THEREFROM, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3; Length 71;
15;
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STREET: 444 South Flower Street, Suite 2000
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100.0%; Score 26;
Best Local Similarity 100.0%; Pred. No. 1
Matches 10; Conservative 0; Mismatche
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Patent No. 6278040
GENERAL INFORMATION:
APPLICANT: Sucov, Henry M.
Evans, Ronald M.
Chien, Kenneth R.
                                                                                                                                                                                                                           US-08-464-514-3
; Sequence 3, Application US/08464514
; Patent No. 6265173
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TELEPAX: (619) 546-9392
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 71 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 444 soc. CITY: Los Angeles STATE: California
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
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39 CXXXXXXXC 48
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STRANDEDNESS: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 48
US-08-802-468-1
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GENERAL INFORMATION:
APPLICANT: BYANS, RONALD M.
APPLICANT: BYANS, MICHAEL B.
APPLICANT: ORO, ANTHONY E.
APPLICANT: SERAVES, WILLIAM A.
APPLICANT: SERAVES, WILLIAM A.
APPLICANT: SERAVES, WILLIAM A.
APPLICANT: YAO, TSO-PANG
TITLE OF INVENTION: ULTRASPIRACLE RECEPTOR
TITLE OF INVENTION: ULTRASPIRACLE RECEPTOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                 COUNTY: USA
COUNTY: USA
COUNTY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,468
FILING DATE: 19-Feb-1997
PRIOR APPLICATION NUMBER: US/08/21,044
FILING DATE: 10-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: REPERENCE/DOCKET NUMBER: 31,192
REFERENCE/DOCKET NUMBER: 91,9749
TELEFAATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: 91,9749
TELEFAATION INFORMATION:
TELEFAATION INFORMATION:
TELEFAATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LINFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 71 aming acids
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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444 South Flower Street, Suite 2000
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MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentur Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 26; DB
; Pred. No. 15;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
TOPOLOGY: linear
;
MOLECULE TYPE: protein
;
FRAGMENT TYPE: internal
;
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-802-468-1
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RESULT 51

1 GS-09-079-570B-1

2 GS-09-079-570B-1

3 GENERAL INFORMATION:
APPLICANT: EVANS, Ronald
APPLICANT: SAEZ, Enrique
TITLE OF INVENTION: GENES IN MAMMALIAN SYSTEMS, AND PRODUCTS RELATED THERETO
TITLE OF INVENTION GENES IN MAMMALIAN SYSTEMS, AND PRODUCTS RELATED THERETO
CURRENT FILING DATE: 1998-05-14

PRIOR APPLICATION NUMBER: US/09/079, 570B
CURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 27

SOFTWARE: PALENTIN VERSION 3.0

SEG ID NO 1

LENGTH: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature

OTHER INFORMATION: Binding domain of the steroid/thyroid hormone superfamily of OTHER INFORMATION: receptor

NAME/KEY: VARIANT

NAME/KEY: VARIANT

COCATION: (1)...(71)

OTHER INFORMATION: Xaa is any amino acid
US-09-079-5708-1
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Sequence 10. 6387673

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BYANS, Ronald M
APPLICANT: BYANS, Ronald M
APPLICANT: BYANS, RONALD
TITLE OF INVENTION: COMPOUNDS USEFUL FOR THE MODULATION OF PROCESSES
TITLE OF INVENTION: MEDIATED BY NUCLEAR HORWONE RECEPTORS, METHODS FOR THE TITLE OF INVENTION: IDENTIFICATION AND USE OF SUCH COMPOUNDS
TITLE OF INVENTION: 1997-05-01
CURRENT APPLICATION NUMBER: US/08/846,881A
CURRENT FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1
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                                                                                          Gaps
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LOCATION: (1)..(71)
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                                Query Match
Best Local Similarity 100.0%; Pred. No. 15;
Matches 10; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                       1 CXXXXXXXX 10
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US-08-846-881A-1
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Fatent No. 6300488
GENERAL INFORMATION:
APPLICANT: Subr. Steven T.
TILLE OF INVENTION: Modified Lepidopteran Receptors
TILLE OF INVENTION: and Hybrid Multi-Functional Proteins for Use in Transcription
TILLE OF INVENTION: and Transgene Expression Regulation
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich
STREET: 4365 Executive Drive, Suite 1600
GTHY: San Diego
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MODUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COPERATING SYSTEM: DOS
SOFTWARE: PASISED for Windows DEMONSTRATION Version 2.0D
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 26; DB 3; Length 71; ilarity 100.0%; Pred. No. 15; Conservative 0; Mismatches 0; Indels
                                                                                                           NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P41 9321
TELEPHONE: (619) 546-4737
TELEPHONE: (619) 546-9392
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 71 amino acids
PRIOR APPLICATION DATA: 07/907,908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E
REGISCRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION:
TELEPHONE: 619-677-1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 71 amino acids
                                          APPLICATION NUMBER: US 07
FILING DATE: 02-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 619-677-1465
                                                                                                                                                                                                                                                                                                                                                     unknown
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXXXXXXXX 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 CXXXXXXXC 48
                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                           TYPE: amino acid STRANDEDNESS: un)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 10; Conserv
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Sequence 1. Application US/08877966B
Sequence 1. Application US/08877966B
Patent No. 6458926
GENERAL INFORMATION:
APPLICANT: Evans, Forman arry M.
APPLICANT: Forman, Barry M.
APPLICANT: Unescono, Kazuhiko
TITLE OF INVENTION: ALLOSTERIC CONTROL OF NUCLEAR HORMONE RECEPTORS NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich
STREET: 4365 Executive Drive, Suite 1600
CITY: San Diego
STREET: A.
ION: (28)...(38)
INFORMATION: each Xaa designates non-conserved amino acids;
INFORMATION: 37-38 are optional residues
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ZIP: 92121
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: Estency for windows DEMONSTRATION Version 2.0D
SOFTWARE: FastEng for windows DEMONSTRATION Version 2.0D
CURRENT APPLICATION NUMBER: US/08/877,966B
TIING DATE: 17-JUN-1997
TIING DATE: 17-JUN-1997
                                                                                               NAME/KEY: VARIANT
LOCATION: (40)
OTHER INFORMATION: 45-47 are optional residues
OTHER INFORMATION: 45-47 are optional residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: VARIANT
LOCATION: (53)...(54)
OTHER INFORMATION: each Xaa designates non-conserved amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (56)...(57)
OTHER INFORMATION: each Xaa designates non-conserved amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: VARIANT
LOCATION: (59)...(60)
OTHER INFORMATION: each Xaa designates non-conserved amino acids
                                                                                                                                                                                                                                            LOCATION: (49)...(51)
OTHER INFORMATION: each Xaa designates non-conserved amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 26; DB
ilarity 100.0%; Pred. No. 15;
Conservative 0; Mismatches
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PPLICATION NUMBER: 08/372,217
FILING DATE: 13-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 CXXXXXXXC 48
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Best Local Similarity
Matches 10; Conserv
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NAME/KEY: VARIANT
                                                                                                                                                                                                                  NAME/KEY: VARIANT
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STATE: C/
COUNTRY:
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US-08-877-966B-1
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                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (23)...(23)
OTHER INFORMATION: each Xaa designates non-conserved amino acids
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OTHER INFORMATION: each Xaa designates non-conserved amino acids
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LOCATION: (14)...(17)
OTHER INFORMATION: each Xaa designates non-conserved amino acids
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OTHER INFORMATION: each Xaa designates non-conserved amino acids
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THER INFORMATION: each Xaa designates non-conserved amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OCATION: (12)...(12)
OTHER INFORMATION: each Xaa designates non-conserved amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (19)...(20)
OTHER INFORMATION: each Xaa designates non-conserved amino acids
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OTHER INFORMATION: each Xaa designates non-conserved amino acids
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US-09-352-816-1

Sequence 1, Application US/09352816

Sequence 1, Application US/09352816

Sequence 1, Application US/09352816

Sequence 1, Application US/09352816

SERENT: Nagy, Laszlo

TITLE OF INVENTION: USE OF RAR ANTAGONISTS AS MODULATORS OF TITLE OF INVENTION: HORMONE MEDIATED PROCESSES

FILE REFERENCE: Salk2060

CURRENT APPLICATION NUMBER: US/09/352,816

CURRENT FILING DATE: 1999-07-13

NUMBER OF SEQ ID NOS: 1

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 15;
Matches 10; Conservative 0; Mismatches 0; Indels
     ; OTHER INFORMATION: Xaa is any amino acid US-08-846-881A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                         1 CXXXXXXX 10
                                                                                                                                                                                                                     39 CXXXXXXXX 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: VARIANT
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IAME/KEY: VARIANT
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LENGTH: 71
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Gaps

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Eichele, Gregor
Thaller, Christina
TITLE OF INVENTION: MEANS FOR THE MODULATION OF PROCESSES
MEDIATED BY RETINOID RECEPTORS AND COMPOUNDS USEFUL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: LOS Angeles
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CUMPLAIL USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOTTWARE: Patentin Release #1.0, Version #1.25

CURRIN DATE: 19-8ep-2002

FILING DATE: 19-8ep-2002

CLASSIFICATION OF CURROWN>

PRIOR APPLICATION NUMBER: US/08/472,817

FILING DATE: 07-UN-1995

FILING DATE: 14-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 26; DB 4; Length 71;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08480967;
Patent No. 6506917
GENERAL INFORMATION:
MANAGELEGATE, David J.
Managelledorf, David J.
Heyman, Richard A.
Boehm, Marcus F.
                                                                                                                                                                                                                                                                                                                                                                                                                                  COCATION: (59)...(60)

OTHER INFORMATION: any amino acid
NAME/KEY: MOD RES

OTHER INFORMATION: any amino acid
NAME/KEY: MOD RES

LOCATION: (67)...(69)

COTHER INFORMATION: any amino acid
OTHER INFORMATION: any amino acid
US-07-672-530C-33
                                                                      NAWE/KEY: MOD RES
LOCATION: (28). (38)
COTHER. INFORMATION: any amino acid
NAME/KEY: MOD RES
LOCATION: (40). (47)
COTHER INFORMATION: any amino acid
NAME/KEY: MOD RES
LOCATION: (49). (51)
COTHER INFORMATION: any amino acid
NAME/KEY: MOD RES
NAME/KEY: MOD RES
NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                  LOCATION: (53)...(54)
OTHER INFORMATION: any amino acid
NAME/KEY: MOD RES
LOCATION: (56)..(57)
OTHER INFORMATION: any amino acid
NAME/KEY: MOD_RES
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                                                     OTHER INFORMATION: any amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXXXXXXXX 10
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US-07-670-530C-33
US-07-670-530C-33
Sequence 33, Application US/07672530C
Patent No. 6492137
GENERAL INFORMATION:
APPLICANT: SUCOV, HENRY M
APPLICANT: UMESONO, KAZUHIKO
TILE OF INVENTION RESPONSE ELEMENT COMPOSITIONS AND ASSAYS EMPLOYING SAME
FILE REFERENCE: 080802/1552
CURRENT APPLICATION NUMBER: US/07/672,530C
CURRENT APPLICATION NUMBER: 07/438,757
FILE REPLING DATE: 1989-11-16
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 33
LENGTH: 71
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                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         ó.
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100.0%; Pred. No. 15;
vative 0; Mismatches 0; Indels
                                                                               SALK 1450-1
NAME: Reiter, Stephen B
REGISTRATION NUMBER: 31,192
REFERENCE DOCKET NUMBER: SALK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (19)..(20)
OTHER INFORMATION: any amino acid
NAME/KEY: MOD RES
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OTHER INFORMATION: any amino acid
NAME/KEY: MOD_RES
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OTHER INFORMATION: any amino acid
NAME/KEY: MOD RES
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OTHER INFORMATION: any amino acid
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OTHER INFORMATION: any amino acid
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THER INFORMATION: any amino acid
                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 71 amino acids
TYPE: amino acid
STRANUEDRESS: single
J. TOPOLOGY: linear
US-08-877-966B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CXXXXXXXC 10
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PRILIMO DATE: 18-20-19 of 760.900

**TILIMO OF TILIMO DATE: 18-20-19 of 760.900

**TILIMO DATE: 18-20-
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### REPERVITY CHOCKE NURSE: P41 9979

**TELECOMMUNICATION MINERAL PAPER PAPER P41 9979

**TELECOMMUNICATION MINERAL PAPER P41 9979

**TELECOMUNICATION MINERAL PAPER P41 9979

**TELECOMMUNICATION MINERAL PAPER P41 9979

**TELECOMUNICATION MINERAL PAPER P41 99
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/note= "May be cleaved off, or if
present, C-terminal must be Arg preceded by 1-29 Xaa's."
                                                                                                                                                                                                                                                          If not, then 61-91
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Patent No. 6395890

GENERAL INFORMATION:
APPLICANT: Sheppers, Stephen R.
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR HOMOLOGS
FILE REFERENCE: 97-75
CURRENT APPLICATION NUMBER: US/09/253,316
CURRENT FILING DATE: 1999-02-19

BARLIER PILING DATE: 1998-02-20

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE: OTHER INFORMATION: connective tissue growth factor family motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
| NAME/KEY: Peptide | LOCATION: 113..122 | LOCATION: 113..122 | COTHER INFORMATION: /note= "If present, up to 8 amino acids of the course in the country of the co
                                                                                                                                                                                                        /note= "If Xaa at position 61 is
L-arginine, then 62-91 are missing. If
C-chain of human or animal proinsulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 18;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "If hydroxy substituted, then peptide terminates at this position."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ION: (32)...(32)
INFORMATION: Xaa is any amino acid or not present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (10)...(11)
OTHER INFORMATION: Xaa is any amino acid or not present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: VARIANT
LOCATION: (34)...(38)
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: VARIANT
LOCATION: (2)...(9)
OTHER INFORMATION: Xaa is any amino acid
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OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 23
LENGTH: 127
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                      NAME/KEY: Peptide
LOCATION: 61..91
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 112
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
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LOCATION: (39)...(40)
                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Peptide
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US-09-253-316-23
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                                                                                                                                                                                                                                                                                                   /note= "Xaa is an amino acid from the group comprising Asn, Gln, Asp, Glu, Gly, Ser, Thr, Ala d Met, and if hydroxy substituted, then peptide terminates at t position."
                                        /note= "If Xaa at position 61 is
L-arginine, then 62-91 are missing. If not, then 61-91 are
C-chain of human or animal proinsulin."
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Patent No. 5728543
GENEAL INFORMATION:
APPLICANT: Dorschug, Michael
APPLICANT: Koller, Klaus-Peter
APPLICANT: Meiwes, Johannes
TITLE OF INVENTION: An Enzymatic Process for the
TITLE OF INVENTION: Conversion of Preproinsulins Into Insulins
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Peptide

LOCATION: 113.122

OTHER INFORMATION: /note= "If present, up to 8 amino oTHER INFORMATION: acids may be missing."

US-08-291-060B-3
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ZIP: 20005-3315
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/291,060B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION: 435
FILING DATE: 08-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Effactory of the control of th
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1300 I Street, N.W.
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 CXXXXXXXX 111
                                                                                                                                                               PEATURE:
NANE/KEY: Peptide
LOCATION: 112
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
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LOCATION: 61..91
OTHER INFORMATION:
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OTHER INFORMATION:
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STREET: 13
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US-08-291-060B-4
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GENERAL INFORMATION:
APPLICANT: Sim_Kim L.
APPLICANT: Sim_Kim L.
APPLICANT: Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM PALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESSED: Knobbe Martens Olson & Bear
STREE: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 19;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     /note= "All or some of residues may
be missing."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "If present, may be missing
nine amino acids."
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,459A
FILING DATE: 07-DEC-1995
CLASSIFICATION: 4355
                                                                        02481.1105-02000
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Sequence 14, Application US/08568459A
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGIEVATION UNMBER: 32,220
REFERENCE/DOCKET NUMBER: 02481
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 408-4366
TELEFAX: (202) 408-4366
TELEFAX: (202) 408-4366
TELEFAX: 137 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,6
                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
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                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1.51
COTHER INFORMATION: VOTHER INFORMATION: FEATURE: NAME/KEY: Peptide LOCATION: 127
OTHER INFORMATION: VOTHER INFORMATION: 1
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CCATION: 128.137
OTHER INFORMATION:
OTHER INFORMATION:
US-08-291-060B-2
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Sequence 2, Application US/08291060B

Sequence 2, Application US/08291060B

Patent No. 5728543

GENERAL INFORMATION:
APPLICANT: Descend, Michael
APPLICANT: Marquardt, Rudiger
APPLICANT: Marquardt, Rudiger
APPLICANT: Marquardt, Rudiger
APPLICANT: Marquardt, Rudiger
TITLE OF INVENTION: An Enzymatic Process for the
TITLE OF INVENTION: Conversion of Preproinsulins Into Insulins
NUMBER OF SEQUENCES:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
CITY: Washington
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 19;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: VARIANT
LOCATION: (107)...(108)
OTHER INFORMATION: Xaa is any amino acid or not present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . LOCATION: (123)...(126)
. OTHER INFORMATION: Xaa is any amino acid or not present
US-09-253-316-23
                                                                                                                                                                             LOCATION: (54)...(54)
OTHER INFORMATION: Xaa is any amino acid or not present
                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (63)...(63)
OTHER INFORMATION: Xaa is any amino acid or not present
                 OTHER INFORMATION: Xaa is any amino acid or not present
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ZIP: 2005-3315
COMPUTER REDABLE FORM:
MEDIUT TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/291,060B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: VARIANT
NOCATION: (110)...(122)
CTHER INFORMATION: Xaa is any amino acid
FEATURE:
                                                                                                                                                                                                                                                                          LOCATION: (56)...(62)
OTHER INFORMATION: Xaa is any amino acid
                                                                                     LOCATION: (42)...(53)
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                             OCATION: (65)...(106)
THER INFORMATION: Xaa is any amino acid
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08-AUG-1994
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT LOCATION: (123)...
                                                                                                                                                    NAME/KEY: VARIANT LOCATION: (54)...
                                                                                                                                                                                                                                                 NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                            NAME/KEY: VARIANT
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APPLICANT: Chitnis, Chetan
APPLICANT: Chitnis, Chetan
APPLICANT: Chitnis, Chetan
APPLICANT: Miler, Louis H.
APPLICANT: Miler, Louis H.
APPLICANT: Su, Xin-zhaun
APPLICANT: Su, Xin-zhaun
APPLICANT: Su, Xin-zhaun
APPLICANT: Wallems, Thomas B.
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                         Query Match 100.0%; Score 26; DB 2; Length 271; Best Local Similarity 100.0%; Pred. No. 25; Matches 10; Conservative 0; Mismatches 0; Indels
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ZIF: 92660
COMPUTER: EDADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EDAP FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EDA FO COMPATIBLE
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE:
CLASSIFICATION NUMBER: US/09/210,288
FILING ADATE:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NH121.1FWDV1
TELEPAX: (619) 235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/09210288
Patent.No. 6392026
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 271 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 CXXXXXXXX 198
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          , ORIGINAL SOURCE:
US-08-487-826B-26
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US-08-568-459A-21
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US-09-210-288-14
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Patent No. 593827

GENERAL INFORMATION:

APPLICANT: Sim, Kim L.

APPLICANT: Chitnis, Chetan

APPLICANT: Chitnis, Chetan

APPLICANT: Miler, Louis H.

APPLICANT: Buller, Louis H.

AP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,826B

FLING DATE: 10-EP-1993

CLASSIFICATION: 435

ATTORNEY/AGBNT INFORMATION:

NAME: Israelsen. Ned

REGISTRATION NUMBER: NIH121.001CP1

TELEPANCE/DOCKET NUMBER: NIH121.001CP1

TELEPANCE/OCKET NUMBER: 35-856

TELEPANCE/OCKET NUMBER: 135-856

TELEPANCE: (619) 235-0176

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 271 amino acids

TYPE: amino acid

TYPE: amino acid

TYPE: Angle
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMONIVINICATION INPORMATION:
TELEPHONE: (619) 235-8550
TELEPAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 14:
SEGUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
TYPE: TYPE: amino acids
TYPE: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        internal
                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 CXXXXXXXX 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO FRAGMENT TYPE: i ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 63
US-08-487-826B-26
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Sequence 21, Application US/09210288
Patent No. 6392026
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Chitnis, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 26; DB 2; Length 311; Best Local Similarity 100.0%; Pred. No. 26; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                        COMPOTER: PLORM:
MEDIUM TYPE: PLORPY disk
MEDIUM TYPE: PLORPY disk
COMPUTER: EMPTORED BY
COMPUTER: EMPTORED BY
SOFTWARE: PRACEDIAL BY
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10.5EP-1993
CLASSIFRCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENDE/DOCKET WUMBER: 29,655
TELECOMMULATION INFORMATION:
TELECOMMULATION INFORMATION:
TELECOMMULATION INFORMATION:
TELECOMMULATION INFORMATION:
TELECOMMULATION FOR SEQ 1D NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ): 620 Newport Center Drive 16th Floor
Newport Beach
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA: US/09/210,288
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 311 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: pept
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: int
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                      92660
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US-09-210-288-21
                                                                                         STATE: C
Sequence 21, Application US/08568459A
Patent No. 5849306
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Olitis, Chetan
APPLICANT: Miler, Louis H.
APPLICANT: Miler, Louis H.
APPLICANT: Wellems, Thomas E.
ITIE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF SEQUENCES: 37
CORRESPONDENCE ADDRESS: 37
CORRESPONDENCE ADDRESSE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STREET: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 33, Application US/08487826B
Patent No. 5993827
GENERAL INFORMATION
APPLICANT: Sim, Kim L.
APPLICANT: Miller, Louis H.
APPLICANT: Miller, Louis H.
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Peterson, David S.
APPLICANT: Peterson, David S.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,459A
FILING DATE: US/DEC-1995
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: BEABLE, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/POCKET NUMBER: 29,655
REFERENCE/POCKET NUMBER: 1010TP1
TELEPHONE: (619) 235-0376
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
FNAMTH: 311 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 311 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL:
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US-08-487-826B-33
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US=08-487-826B-29
Sequence 29, Application US/08487826B
Sequence 29, Application US/08487826B
Sequence 29, Application US/08487826B
Sequence 29, Application
Sequence 29, Application
Sequence 29, Application
APPLICANT: Sim, Kim L.
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Peterson, David S.
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: AND PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
STREET: 620 Newport Center Drive 16th Floor
STREET: 620 Newport Center Drive 16th Floor
STREET: Galifornia
COUNTRY: US
STREET: 225 CARESTONERS STREET
STREET: 225 CARESTONERS STREET
STREET: 225 CARESTONERS STREET
STREET: 225 Newport Center Drive 16th Floor
STREET: 225 CARESTONERS STREET
STREET: 225 CARESTONERS 
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Best Local Similarity 100.0%; Score 26; DB 2; Length 324;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 10; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILNG DATE: US-0894
FILNG DATE: US-089-1993
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: BTSAENCE/POCKET NUMBER: NH121.001CP1
TELEPHONE: (619) 235-850
TELEPHONE: (619) 235-0176
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 334 amino acids
INFORMATION: A mingle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 26; DB 2; ilarity 100.0%; Pred. No. 27; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           internal
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                         internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CXXXXXXXX 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
                                                 ; ANTI-SENSE: NO
; FRAGMENT TYPE: i
; ORIGINAL SOURCE:
US-08-568-459A-17
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 69
US-08-487-826B-29
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APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Chitnis, Chetan
APPLICANT: Chitnis, Chetan
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Su, Xin-zhaun
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: AND PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 311; 26;
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COUNTRY: US
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/568,459A
FILING DATE: 07-DEC-1995
CLASSIFICATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: 29,655
REFERENCE/DOCKET NUMBER: 29,655
REFERENCE/DOCKET NUMBER: 19,655
REFERENCE/DOCKET NUMBER: 19,656
REGISTATION NUMBER: 23,655
REFERENCE/DOCKET NUMBER: 19,656
REGISTATION NUMBER: 19,656
REGI
                                                                  NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REGISTRATION NUMBER: 36,516
REBERENCE FOCKET NUMBER: NIH121.1FWDV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
RELEPAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 311 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 26;
Best Local Similarity 100.0%; Pred. No. 2
Matches 10; Conservative 0; Mismatche
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 311 amino acids
TYPE: amino acids
TYPE: amino acid
TYPE: amino aci
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us-10-046-922-33.open.rai

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195-09-210-2880

Sequence 17, Application US/09210288

PAPLICANT. Sim, Kin Chean
APPLICANT. Sim, Kin Chean
APPLICANT. Sim, Kin Chean
APPLICANT. Millar Louis H
APPLICANT. Millar 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Best Local Similarity 100.0%; Pred. No. 27;
Matches 10; Conservative 0; Mismatches 0; Indels
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RESULT 70
US-09-210-288-17
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Search completed: May 4, 2004, 07:13:57 Job time: 24 secs

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Fri May
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May 7, 2004, 06:21:40 ; Search time 13.44 Seconds (without alignments) 30.730 Million cell updates/sec
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                             389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                     BLOSUM62XX
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                              US-10-046-922-68
39
1 GYWXXXWX 8
                                                                                                                                                                                                                              Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                                                                         Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 1668, Apply Sequence 2, Apply Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 13, Appli Sequence 13, Appli Sequence 2, Appli Sequence 336, Appli Sequence 336, Appli Sequence 336, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 336, Appli Sequence 2, Appli Sequence 2, Appli Sequence 13, Appli Sequence 13, Appli Sequence 116, Appli Sequenc
SUMMARIES ID	US-09-350-641C-1668 US-08-990-888-4 US-08-990-888-4 US-08-472-240A-3 US-08-472-240A-3 US-08-353-400-27 US-08-353-400-27 US-08-353-400-27 US-08-353-400-27 US-09-388-788-2 US-09-388-788-2 US-09-388-788-2 US-09-38-641-1 US-09-125-641-2 US-08-465-339 US-08-465-339 US-08-465-339 US-08-465-339 US-08-465-339 US-08-465-339 US-08-465-338-334 US-08-465-338-334 US-08-125-641-3 US-08-465-338-334 US-08-465-338-334 US-08-465-338-334 US-08-465-338-334 US-08-125-641-3 US-08-465-338-334 US-08-465-338-334 US-08-125-641-16 US-09-125-641-16 US-08-125-641-16 US-08-125-641-16 US-08-125-641-3 US-08-125-641-16 US-08-125-641-16 US-08-125-641-16 US-08-125-641-16 US-08-125-641-16
DB	,   a a a a a w u u a a a a a a a a a a a a
% Query Match Length	9889 1 9889 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
% Query Match	6 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
Score	   1   0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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29 24 61.5 11 1 US-08-465-391A-315 30 24 61.5 11 1 US-08-465-391A-315 31 24 61.5 11 1 US-08-465-391A-321 32 24 61.5 11 1 US-08-465-391A-322 33 24 61.5 11 1 US-08-465-391A-323 34 24 61.5 11 1 US-08-465-391A-324 35 24 61.5 11 1 US-08-465-391A-345 37 24 61.5 11 1 US-08-465-391A-345 38 24 61.5 11 1 US-08-465-391A-345 40 24 61.5 11 1 US-08-465-391A-345 41 24 61.5 11 1 US-08-465-391A-345 42 61.5 11 1 US-08-465-391A-345 43 24 61.5 11 1 US-08-465-391A-345 44 21 11 US-08-465-391A-345 45 24 61.5 11 1 US-08-465-391A-34 45 24 61.5 11 US-08-465-391A-34	Sequence 315, App Sequence 316, App Sequence 321, App Sequence 321, App Sequence 323, App Sequence 323, App Sequence 334, App Sequence 337, App Sequence 337, App Sequence 343, App Sequence 343, App Sequence 345, App Sequence 345, App Sequence 345, App Sequence 346, App Sequence 346, App Sequence 346, App Sequence 346, App Sequence 346, App Sequence 349, App Sequence 349, App Sequence 349, App Sequence 349, App	D PHARMACOKINETIC	Length 8; ; Indels 0; Gaps 0;	
RD Land and a land a la	24 61.5 111 1 U U U U U U U U U U U U U U U U	RESULT 1  US-99-360-64IC-1668-  Sequence 1668, Application USA0935064IC  SERBEAL INFORMATION:  APPLICANT: BAINEY-R.  APPLICANT: Anner, M.  PROFICANT: Anner, M.  PRICA INVENTION: PROPERTIES  FILE REFERENCE: 7372-067  CURRENT APPLICATION NUMBER: US/09/350,641C  CURRENT APPLICATION NUMBER: 09/315,304  PRIOR FILING DATE: 1999-07-09  PRIOR PLILING DATE: 1999-05-20  PRIOR FILING DATE: 1999-05-20  PRIOR FILING DATE: 1999-05-20  WUMBER OF SEQ ID NOS: 1757  SEQ ID NO 1668	LENGTH: 8  TYPE: PRI  ORGANISH: HIV-1  FEATURE: NAME/KEX: SITE: NAME/KEX: SITE	pplication US/0899088 87879 MATION: lume, Arthur J. rissette, Renee arcano, Juan andecki, Wlodeck S. ang, Fauline M.

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14 WXXXW 18
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76 GYWX 79
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                                                                                                                                                                                                 US-08-936-165A-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
US-08-472-240A-2
TITLE OF INVENTION: Assays For Compounds Which Bind Growth Hormone Receptor FILE REFERENCE: 2596-4002
CURRENT APPLICATION NUMBER: US/08/990,888B
CURRENT FILING DATE: 1997-12-15
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin Ver. 2.1
SED ID NO 4
LENGTH: 16
                                                                                                                                                                                                                                                          PEATURE:
OTHER INFORMATION: consensus sequence, wherein X1 is S, R, T, N, H,
OTHER INFORMATION: or A, X2 is L, W, or P, X3 is G, A, V, P, Q, E, or
OTHER INFORMATION: R, X4 is V, I, A, L, D, E, P, or F; X5 is T, G, S,
OTHER INFORMATION: R, K, N, A, L, or W; X6 is Y, W, F, or Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                  REATURE:
OTHER INFORMATION: X7 is L, V, or I; X8 is A, T, S, V, W, or D; X9
US-08-990-888-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Knowless, David
APPLICANT: Knowless, David
APPLICANT: Lonetto, Michael
APPLICANT: Nicholas, Richard
APPLICANT: Reichard, Richard
APPLICANT: Reichard, Richard
APPLICANT: Rosenberg, Martin
APPLICANT: Rosenberg, Martin
APPLICANT: Ward, Undith
TITLE OF INVENTION: No. 6348582el Prokaryotic Polymucleotides,
NUMBER OF SEQUENCES: 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.1%; Score 25; DB 4; Length 16; 100.0%; Pred. No. 18+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM ILE:
COMPUTER: IDENCATE
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCTHARE: PERSENE for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,165A
FILING DATE: 24-SEP-1997
CLASSIFICATION NUMBER: 60/027,032
APPLICATION NUMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: 61-02710 INFORMATION:
REFERENCE/DOCKET NUMBER: 28-891
REGISTRATION NUMBER: 28-891
REGISTRATION NUMBER: 28-891
RESISTRATION NUMBER: 28-891
TELESPAN: 610-270-4478
TELEFAX: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 534
CORRESPONDENCE ADDRESS:
ADDRESSES: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 262, Application US/08936165A
Patent No. 6348582
GENERAL INPORMATION:
APPLICANT: Black, Michael
APPLICANT: Burnham, Martin
APPLICANT: Hodgson, John
                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 WXXXW 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 WXXXW 7
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US-08-936-165A-262
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                                                                                                                                                                                                                                                                                                                                                                                                          Query March
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08472240A
Patent No. 6284248
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: GRIEF HYBRID,
TITLE OF INVENTION: GRIEF HYBRID,
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: United States
COUNTRY: United States
ZIP: 22313-1404
COUNTRY: United States
ZIP: 22313-1404
COMPUTER: United States
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CONTREME PRICATION DATA:
APPLICATION NUMBER: US/08/472,240A
RPLICATION NUMBER: US/08/472,240A
RPLICATION NUMBER: US/08/472,240A
RPLICATION NUMBER: US/08/472,240A
RPLICATION NUMBER: US/07/956,483
FILING DATE: 31-DEC-1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01753-055
TELECOMMUNICATION INFORMATION:
TELECOMMUNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 887 amino acids
TYPE: amino acid
STRANDEDNESS: not releva:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: not relevant MOLECULE TYPE: peptide
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 amino acids
                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY; Protein
; LOCATION: 1..854
US-08-472-240A-2
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WESULO 13.750B-38
Sequence 38, Application US/08753750B
Sequence 38, Application US/08753750B
Sequence 38, Application US/08753750B
Sequence 38, Application GEOSGE
GENERAL INFORMATION:
APPLICANT: Lo, Reggie Y.C.
APPLICANT: Schryvers, Anthony B.
TITLE OF INVENTION: PARSTERRELH HARMOLYTICA AND VACCINES CONTAINING THE SAME
TITLE OF INVENTION: PASTERRELL HARMOLYTICA AND VACCINES CONTAINING THE SAME
TITLE OF INVENTION: PASTERRELL 10.05
CURRENT TRING DATE: 1995-11-29
CURRENT FILING DATE: 1995-12-01
PRIOR FILING DATE: 1995-12-01
PRIOR FILING DATE: 1995-12-01
PRIOR FILING DATE: 1995-12-01
NUMBER OF SEQ ID NOS: 68
SEQ ID NOS: 68
LENGTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Salandarian | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.5%; Score 24; DB 1; Length 5; 100.0%; Pred. No. 3e+05; tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 3e+05;
:ive 0; Mismatches 0
PILING DATE:
CLASSIPECATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION ONDER: GB 9324819.3
FILING DATE: 03-DEC-1993
PRIOR APPLICATION NUMBER: GB 9411089.7
APPLICATION NUMBER: GB 9411089.7
FILING DATE: 03-UNM-1994
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amilio acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Pasteurella haemolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear;
; MOLECULE TYPE: protein
US-08-353-400-27
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                    WESULY S

SEQUENCE 3. Application US/08472240A

Patent No. 6284913

SEQUENCE 3. Application US/08472240A

Patent No. 6284910

FAPLICANT: KIENY MARIE-Paule

TITLE OF INVENTION: MARIE-Paule

TITLE OF INVENTION: SPIC OVERIANT

NUMBER OF SEQUENCES: 29

CORRESSER: BURNS, DOANE, SWECKER & MATHIS

STREET: P.O. Box 1404

CITY: Alexandria

STREET: VITALIA

STREET: P.O. Box 1404

COMPUTE: United States

ZIP: 22313-140

COMPUTE: INP COMPUTE: US/08/472,240A

STREETIN PERCATION DATA:

MEDIUM TYPE: Floppy disk

COMPUTE: INP COMPUTE: US/08/472,240A

PILLAGATION NUMBER: US/08/472,240A

PILLAGATION NUMBER: US/08/472,240A

APPLICATION NUMBER: US/08/472,240A

TELESPAN: ROBIN L.

REGISTRATION NUMBER: 35,030

REGISTRATION NUMBER: 35,030

TELESPAN: (703) 836-620

TELEPHONE: (703) 836-620

TELEPHONE: (703) 836-620

TELEPHONE: (703) 836-031

INPORMATION FOR SEQ ID NO: 3:

ENDORMATION FOR SEQ ID NO: 3:

ENDORMATION FOR SEQ ID NO: 3:

TELEPHONE: OF CAMPANDER

TOPOLOGY: NOT CALEVANT

NOLECULE TYPE: peptide

FRATURE: FRATURE: FRATURE

FRATURE: FRATURE: PERCHANT
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; Sequence 27, Application US/08353400
; Patent No. 5665357
; GENERAL INFORMATION:
; TITLE OF INVENTION: PROTEINS
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; COMPUTER: IBM PC compatible
; COMPUTER: PatentIN Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.1%; Score 25; DB 3; Length 906; 100.0%; Pred. No. 3.9e+03; ive 0; Mismatches 0; Indels
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Matches 5; Conservative
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US-08-472-240A-3
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US-08-353-400-27
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TYPE: PRT ORGANISM: Artificial Sequence
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SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Modified-site
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Best Local Similarity
Matches 3; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: IV
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US-08-586-670A-17
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18-09-388-788-2
18-09-388-788-2
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Ouery Match
Best Local Similarity 10:0.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels
Query Match 61.5%; Score 24; DB 6; Length 5; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 3; Conservative 0; Mismatches 0; Indels
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ZIP: 94105-1492
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OMPUTER: IBW PC compatible
OMPUTER: IBW PC compatible
OMPUTER: IBW PC compatible
OMPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PRECENTIN Release #1.0, Version #1.25
CURRENY APPLICATION DATA:
FILING DATE: 19910620
CLASSIFICATION NUMBER: US 07/718,577
FILING DATE: 20-UN-1990
ATTORNEY/ABOUT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REPERENCE/DOCKET NUMBER: 11509-25-1
TELECHONE: (415) 326-2400
SUNDORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTER STICS:
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/0718577
Patent No. S432018
GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Cwirla, Steven E.
APPLICANT: Garrett, Ronald W.
TITLE OF INVENTION: PEFTIDE LIBEARY AND
TITLE OF INVENTION: SCREENING SYSTEMS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Steuart Street
GITTY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESS: single
linear
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US-07-718-577-6
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0; Gaps
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OTHER INFORMATION: /label= Variant residues
OTHER INFORMATION: /note= "Phe is in the D conformation and is
OTHER INFORMATION: linked to DTPA;
                                                                                                                                                                                                                                                                                                                                                                                                                                h Similarity 100.0%; Pred, No. 3e+05; 3; Conservative 0; Mismatches 0; Indels
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Patent No. 6241965
GENERAL INFORMATION:
APPLICANT: MCBride, William
APPLICANT: Dean, Richard T.
TITLE OF INVENTION: Somatostatin Derivatives
TITLE OF INVENTION: And their Radiolabeled Froducts
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
STREET: 10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTY: USA

ZIP: 6666

COMPUTER READABLE FORM:
MEDIUM TYPE: Floopy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/586,670A
FILING DATE: 22-APR 1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,385-DD
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000
TELEFAX: 312-715-134
                   FILE REFERENCE: 21459/90101
CURRENT APPLICATION NUMBER: US/09/388,788
CURRENT FILING DATE: 199-09-02
NUMBER OF SEQ ID NOS: 12
SOSTWARE: Patentin Ver. 2.1
SEQ ID NO. 2
TITLE OF INVENTION: PLANTS
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RESULT 13
US-09-125-641-2
US-09-125-641-1
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       /label= Variant residues
/note="The Phe is in the D conformation; Xaa
/note="The Phe is in the D conformation; Xaa
D conformation;
                                                                                                                                                                                                                                                                    /label= Variant residues
/note= "The carboxyl group of the C-terminal
Thr is reduced to an alcohol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
US-09-125-641-1
US-09-125-641-1
Sequence 1, Application US/09125641
Fatent No. 6810297
GENERAL INFORMATION:
APPLICANT: Krieck, Franz
APPLICANT: Krieck, Franz
TITLE OF INVENTION: Peptide Immunogens For Vaccination
TITLE OF INVENTION: Against and Treatment of Allergy
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6610297artis Corporation
STREET: 564 Morris Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 61.5%; Score 24; DB 3; Length 8; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 3; Conservative 0; Mismatches 0; Indels
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STR...
STREE: New Jell...
COUNTR: U.S.A.

COMPUTE: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
COMPUTER: IBM PC compatible
COMPUTER: INFORMATION:
COMPUTER: COMPUTER: A POOL 196
COMPUTER: COMPUTER: A POOL 
   OTHER INFORMATION: /label=
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EBATURE:
NAMME/KEY: Modified-site
OCHER INFORMATION: /label=
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MOLECULE TYPE: peptide
HYPOTHEICAL: YES
ANTI-SENSE: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  internal
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Sequence 2, Application US/09125641

Sequence 1, Calour 2, Calour 2, Calour 3, 
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Query Match
61.5%; Score 24; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels
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REGISTRATION NUMBER: 36,134
REPERBNCF JOCKET NUMBER: 4-900-9862/A/NFI/PCT
TELEPHONE: (908) 522-6923
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: internal
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STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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ANTI-SENSE: N
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Westurn 14

Westurn 15, 7024-13

Sequence 13, 7024-13

Sequence 13
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score:

Title: Perfect :

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum Maximum

Database

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Sequence 1668, Application US/09350641C

Sequence 1668, Application US/09350641C

Patent No. 6656906

GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Guthrie, K.

APPLICANT: Menuka, G.

APPLICANT: Menuka, G.

APPLICANT: Lambert, D.

TITLE OF INVENTION: HYERID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

TITLE OF INVENTION: HYERID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

TITLE OF INVENTION: HYERID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

TITLE OF INVENTION: HYBRE 1990-1000

FILE REFERENCE: 7872-067

CURRENT FILING DATE: 1990-05-20

PRIOR FILING DATE: 1990-05-20

PRIOR FILING DATE: 1990-05-20

PRIOR FILING DATE: 1990-05-20

PRIOR FILING DATE: 1990-05-20

NUMBER OF SEQ ID NOS: 1757

SOFTWARR: FRALEXQ for Windows Version 3.0
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US-08-465-391A-315
US-08-465-391A-320
US-08-465-391A-321
US-08-465-391A-322
US-08-465-391A-323
US-08-465-391A-323
US-08-465-391A-334
US-08-465-391A-338
US-08-465-391A-345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
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; other information: Xaa=unknown amino acid
US-09-350-641C-1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/0899088BB
Patent No. 639879
GENERAL INPORMATION:
APPLICANT: Blume, Arthur J.
APPLICANT: Brissette, Renee
APPLICANT: Carcamo, Juan
APPLICANT: Tang, Pauline M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.8%; Scc...
100.0%; Pre
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 WXXXW 7
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              TYPE: PRT
ORGANISM: HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: SITE
LOCATION: (1)...
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US-09-350-641C-1668
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US-08-990-888-4
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3, Appli
19, Appl
927, App
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                                                                                                                                                                                                                                               7, 2004, 06:21:40 ; Search time 11.76 Seconds (without alignments) 30.730 Million cell updates/sec
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/cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfles1.pep:*
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- 2004 Compugen Ltd.
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US-08-990-888-4
US-08-472-240A-3
US-08-472-240A-3
US-08-472-240A-3
US-08-472-240A-3
US-08-473-40A-3
US-08-753-750B-38
5188431-15
US-08-753-750B-38
5188-788-2
US-09-125-641-2
US-09-125-641-2
US-08-463-52A-13
US-09-125-641-2
US-08-465-391A-336
US-08-465-391A-336
US-08-465-391A-336
US-08-465-391A-336
US-08-465-391A-336
US-08-465-391A-336
US-08-465-761-3
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US-09-125-641-19
US-09-428-082E-927
US-08-190-788A-116
US-08-383-474B-121
US-08-465-391A-116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            389414 segs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                      protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                     GenCore
Copyright (c) 1993
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DB seq length: 2000000000
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38
1 GYWXXXW 7
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Score

Result No.

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90 amino acids
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Best Local Similarity 100.
Matches 4; Conservative
                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                       TYPE: amino acid
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-936-165A-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-472-240A-2
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TITLE OF INVENTION: Assays For Compounds Which Bind Growth Hormone Receptor FILE REFERENCE: 2598-4002
CURRENT APPLICATION NUMBER: US/08/990,888B
CURRENT FILING DAIE: 1997-12-15
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: consensus sequence, wherein X1 is S, R, T, N, H,
OTHER INFORMATION: consensus sequence, wherein X1 is S, R, V, P, Q, E, or
OTHER INFORMATION: R, X4 is V, I, A, L, D, E, P, or F; X5 is T, G, S,
OTHER INFORMATION: R, K, N, A, L, or W; X6 is Y, W, F, or Q;
FEATURE:
OTHER INFORMATION: X7 is L, V, or I; X8 is A, T, S, V, W, or D; X9
US-08-990-888-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Discolar, Michael APPLICANT: Discolar, Michael APPLICANT: Pratt, Julie APPLICANT: Reichard, Richard APPLICANT: Reichard, Richard APPLICANT: Reschberg, Martin APPLICANT: Ward, Judith TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides, TITLE OF INVENTION: Polypeptides and Their Uses TITLE OF SEQUENCES: 534 CORRESPONDENCE ADDRESS: 634 CORRESPONDENCE ADDRESS: ADDRESSE: SmithKline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia STREET: PA COUNTRY: USA ZIP: 19406-0339 COUNTRY: USA ZIP: 19406-0339 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 65.8%; Score 25; DB 4; Length 16; Best Local Similarity 100.0%; Pred. No. 1e+02; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,165A
FILING DATE: 24.5EP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/027,032
FILING DATE: 24.5EP-196
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R. REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50549
TELEDPHONE: 610-270-4478
TELEDPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 262, Application US/08936165A
Patent No. 6348582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Black, Michael
Burham, Martin
Hodgen, John
Knowles, David
Lonetto, Michael
Nicholas, Richard
Pratt, Julie
Reichard, Richard
Rosenberg, Martin
Ward, Judith
                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 WXXXW 15
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General Coal Similarity 100.00; Fred, No. 4.9e-09; Indels 0; Gaps 0; Marches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Or 1 GrWX 4

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Gaps

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Sequence 38, Application US/08753750B
Patent No. 6610506
GENERAL INFORMATION:
APPLICANT: Lo, Reggie Y.C.
APPLICANT: Schryvers, Anthony B.
APPLICANT: Potter, Andrew A.
TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME FILE REFERENCE: A3762 021645.0105
FILE REPERENCE: A3762 021645.0105
CURRENT APPLICATION NUMBER: US/08/753,750B
CURRENT APPLICATION NUMBER: US/08/753,750B
FRIOR PILING DATE: 1996-11-29
PRIOR PILING DATE: 1995-12-01
PRIOR FILING DATE: 1995-12-01
PRIOR FILING DATE: 1995-12-01
SOFTWARE: FastEEQ for Windows Version 4.0
SOFTWARE: FastEEQ for Windows Version 4.0
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CURRENT APPLICATION DATA:
APPLICATION NESTS: 11-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.2%; Score 24; DB 1; Length 5; 100.0%; Pred. No. 3e+05; cive 0; Mismatches 0; Indels
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100.0%; Pred. No. 3e+05;
tive 0; Mismatches (
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9324819.3
FILING DATE: 03-DEC-1993
FILING DATE: 03-DEC-1993
FILING DATE: 03-DEC-1993
FILING DATE: 03-DEC-1994
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Pasteurella haemolytica
US-08-753-750B-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 3, Conservative
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                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear; MOLECULE TYPE: protein US-08-353-400-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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;Patent No. 5185431
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US-08-753-750B-38
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5185431-15
                                                                                                                                                                                                                                                                                                                      LENGTH:
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| Patent No. 566537
| GENERAL INFORMATION:
| APPLICANT:
| TITLE OF INVENTION: PROTEINS |
| COMPUTER READABLE FORM: |
| MEDIUM TYPE: Floppy disk |
| COMPUTER: PATENTION OF SECTION OF SECTION #1.25 (EPO) |
| GURRENT APPLICATION NUMBER: US/08/353,400 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 65.8%; Score 25; DB 3; Length 906; Best Local Similarity 100.0%; Pred. No. 3.9e+03; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 906 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) NAME/KEY: Protein ; LOCATION: 1..873 US-08-472-240A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 WXXXW 18
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US-08-353-400-27
                                                                     RESULT 5
US-08-472-240A-3
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Gaps

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TITLE OF INVENTION: PLANTS
FILE REFERENCE: 21459/90301
CURRENT APPLICATION NUMBER: US/09/388,788
CURRENT FILING DATE: 1999-09-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: IL
RY: USA
60606
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                                                                                 Gaps
                          63.2%; Score 24; DB 6; Length 5;
100.0%; Pred. No. 3e+05;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.2%; Score 24; DB 1; Length 6; 100.0%; Pred. No. 3e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                        US-U/-718-577-6

Sequence 6, Application US/07718577

Sequence 7, Application US/07718577

Patent No. 5432018

GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Darrett, Ronald W.
TITLE OF INVENTION: SCREENING SYSTEMS
CORRESPONDENCES: 22
CORRESPONDENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSED: Tower
GITY: San Francisco
STREET: One Market Plaza, Steuart Street
STREET: ONE MARKET IN TRANCISCO
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: IBM PC compatible
OPERATION NUMBER: US/07/718,577
TILING DATE: 19910620
TILING DATE: 19910620
ATTORNEY/AGENT INFORMATION:
NUMBER: SMICH, William M.
REGISTRATION NUMBER: 11509-25-1
TELEPAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 maino acide
TTREE AMINO ACID
STRANDENCE AMINO ACID
STRANDENCE AMINO ACID
STRANDENCE AMINO ACID
STRANDENCE
                    Query Match
Best Local Similarity 100.
Matches 3, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                RESULT 9
US-07-718-577-6
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COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
CONFUTER: IBW FC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Perentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/586,670A
FILING DATE: 22-APR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6241965nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,385-DD
TELEPONNUMICATION HOWERH: 92,385-DD
TELEPONNUMICATION HOWERH: 92,385-DD
TELEPONNUMICATION HOWERHING:
TELEPON TELEPONE SEG ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 maino acid
TOPOLOGY: 1inea:
MOLECULE TYPE: peptide
FRATURE:
MOLECULE TYPE: peptide
FRATURE:
NOAME/KEY: Modified-site
LOCATION: 1...2
OTHER INFORMATION: /label= Variant residues
OTHER INFORMATION: /label= Variant in the D conformation and is
COTHER INFORMATION: /label= "Phe is in the D COTHER INFORMATION: /label= NAME/KEY: Modified-site
LOCATION: 1..4
LOCATION: 1..4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein
OTHER INFORMATION: Construct
US-09-388-788-2
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-06-586-670A-17
US-06-586-670A-17
Sequence 17, Application US/08586670A
Fatent No. 6241965
GENERAL INFORMATION
APPLICANT: McBride, William
APPLICANT: Dean, Richard T.
TITLE OF INVENTION: Sometostatin Derivatives
TITLE OF INVENTION: And their Radiolabeled Products
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Banner & Witcoff, Ltd.
STREET: 10 Scuth Wacker Drive, Suite 3000
CITY: Chicago
STATE: IL
COUNTRY: USA
                                                                                                                                                                                               Length 7;
                                                                                                                                                                                            Score 24; DB 4;
; Pred. No. 3e+05;
                                                                                                                                                                                               Query Match 63.2%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 3e4 Matches 3; Conservative 0; Mismatches
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Gaps
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                                                       63.2%; Score 24; DB 4; Length 8;
100.0%; Pred. No. 3e+05;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09125641
Patent No. 6610297
GENERAL INFORMATION
TITLE OF INVENTION: Peptide Immunogens For Vaccination
TITLE OF INVENTION: Against and Treatment of Allergy
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: No. 6610297artis Corporation
STREET: 564 Morris Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACIDEACSAE:
STREET: S64 MORTIS Avenue
CITY: Summit
STATE: Now Jersey
COUNTRY: U.S.A.
ZIP: 07901

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Dam PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/125,641
FILING DATE: 12-AUG-1998
CLASSIFICATION DATE: US/09/125,641
FILING DATE: 22-FEB-1997
PRIOR APPLICATION DATE: BEB-1997
RILING DATE: 22-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: FERTEACO, GREGOTY D.
REGISTRATION NUMBER: B 96,134
REFERENCE/DOCKET NUMBER: 36,134
REGISTRATION NUMBER: 36,134
REFERENCE/COMMINICATION INFORMATION:
TELESPHONE: (908) 522-6923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (908) 522-69:
TELEFAX: (908) 522-6923
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 3; Conservative
                                                             Query Match 63.2
Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
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                                                                                                                                                                                1 GYW 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-125-641-2
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         US-09-125-641-1
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      /label= Variant residues
/note= "The Phe is in the D conformation; Xaa
is L-4-chlorophenylalanine; the Trp is in the
D conformation,
OTHER INFORMATION: /label= Variant residues
CTHER INFORMATION: /note= "The Phe is in the D conformation; Xaa
CTHER INFORMATION: is L-4-chlorophenylalanine; the Trp is in the
COTHER INFORMATION: D conformation;
FRATURE:
NAME/KEY: Modified-site
LOCATION: 7..8
CTHER INFORMATION: /label= Variant residues
CTHER INFORMATION: /note= "The carboxyl group of the C-terminal
US-08-586-670A-17
                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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US-09-125-641-1

US-09-125-641-1

US-09-125-641

Parent No. 6610297

GENERAL INPORMATION:

APPLICANT: Stadler, Beda

TITLE OF INVENTION: Peptide Immunogens For Vaccination

STRESPONDENCE ADDRESS:
ADDRESSE: ADDRESS:
ADDRESSE: New Jersey

COUNTY: Sumit Vo. 64.0237axtis Corporation

STRET: New Jersey

COUNTY: U.S.A.

ZIF: New Jersey

COUNTY: U.S.A.

ZIF: OF 901

CONTYR: U.S.A.

ZIF: OF 902

ZIF: OF 902

ZIF: OF 902

ZIF: OF 902

ZIF: OF 903

ZIF: OF 90
                                                                                                                                                                                                                                                                                                                                                      63.2%; Score 24; DB 3; Length 8; larity 100.0%; Pred. No. 3e+05; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION: (908) 522-6923
TELERAX: (908) 522-6923
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TENGTH: 8 amino 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         internal
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
-hea 3; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GYW 3
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Search completed: May Job time: 12.76 secs
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Patent No. 6083743

GENERAL INFORMATION:
APPLICANT: CHONG, Pele
APPLICANT: THOMAS, Wayne
APPLICANT: LOCSMORE, Sheena
APPLICANT: LOCSMORE, Sheena
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
MINMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIM & MCBUTCH
ADDRESSEE: SIM & M
                                                                                                                                                                                                  APPLICANT: THOMAS, Wayne
APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: YANG, Yan Ping
APPLICANT: YANG, Yan Ping
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
APPLICANT: FILE MICHEL
APPLICANT: TOTONTO
GUTY: TOTONTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.2%; Score 24; DB 3; Length 9;
100.0%; Pred. No. 3e+05;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: CONTEXT
CONTEXT: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/433,522A
FILING DATE: 12-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: STEATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-434 MIS:jb
TELEPHONICATION INFORMATION:
TELEPHONE: (416) 595-1165
INPORMATION FOR SEQ ID NO: 13;
SEQUENCE CHARACTERISTICS:
LENGTH: 9 maino acids
LENGTH: 9 maino acids
LENGTH: 9 maino acids
LENGTH: 9 maino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Sim & McBurney
STREET: 6TH Floor, 330 University Avenue
RESULT 14
18-08-433-522A-13
Sequence 13, Application US/08433522A
Patent No. 6013514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 63.2
Best Local Similarity 100.
Matches 3; Conservative
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STRANDEDNESS: single
; TOPOLOGY: linear
US-08-433-522A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ontario
: Canada
                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Tor
STATE: On
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-09-135-166-13
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COMPUTER: READEL FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: 1EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: 1EM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/135,166
FILING DATE: 12-SEP-1995
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/433,522
FILING DATE: 12-SEP-1995
CLASSIFICATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 1038-829 MIS:jb
FELENGENDRICATION INFORMATION:
TELEPHORE: (416) 595-1155
TELEFAX: (416) 595-1165
TELERACITE AMINOBER: 1038-829 MIS:jb
TELERACITE AMINOBER: 1038-829 MIS:jb
TELERACITE AMINOBER: 1038-829 MIS:jb
TELERACITE AMINO acid
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: Amino aci
```

us-10-046-922-68.open.rsp

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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May 7, 2004, 06:21:40 ; Search time 7.68 Seconds (without alignments) 54.240 Million cell updates/sec Run on:

using sw model

OM protein - protein search,

US-10-046-922-68 39 1 GYWXXXWX 8 Title: Perfect score: Sequence: Scoring table:

BLOSUM62XX Gapop 10.0 , Gapext 0.5

141681 segs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	ption							arabidops						synechocy									cavia porce					escherichia				arabidopsi		chlorobium
	Description	P02885	P83557	P83558	P36493	P33391	<u> </u>	P42354	P28804	P82025	P21224	P77242	P27360	P74794	P20553	P22597	P70742	P19034	034654	050387	083053	P27389	Q922r5	P33622	Osfsu9	P75202	P06759	P39284	P29763	P20088	097686	080594	P10024	Q8kam7
SUPPLAKIES	ID	SILU RHIPU	TXM1_MACGS	TXM2 MACGS	RK32_LYCES	HMC4_DESVH		RK32_ARATH	RK32_SPIOL	IOTA_GONVI	YHLB STAAU	ESSD_ECOLI	VLYS_BPP21	Y738_SYNY3	YVDI VACCC	UL43_HSVE4	DSRD_ARCFU	APC2_BOVIN	YODI BACSU	YX58 MYCTU	Y008 TREPA	VPM_BPPRD	APC3 CAVPO	1 APC3 MOUSE	YT45_COREF	YF78 MYCPN	APC3_RAT	YJEO ECOLI	RLA1_CHLRE		GON2 SUNMU	Y103_ARATH	YGI3_BACTU	RL20_CHLTE
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	Length	30	38	40	44	47	50	51	56	62	67	71	71	72	74	16	77	79	83	85	68	06	16	თ თ	<u>თ</u>	100	101	104	107	108	110	110	114	115
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Q98qv0 mycoplasma P01811 mus musculu O63850 sarcophyton Q35100 metridium s Q35100 metridium s Q3520 metridium s P1856 african swi P26707 african swi P26707 african swi P26708 african swi P26708 african swi P267108 african swi P267108 african swi P267108 african swi P267108 african swi P39522 bacteriopha			re) Mucorales, Mucoraceae,	antimicrobial peptide from ial agent produced by the llus in liquid culture; it is revia at the level of RNA	CRC64;	1; Length 30; ' 0; Indels 0; Gaps 0;		A. (ce) (a; Arachnida; Araneae; TISSUE SPECIFICITY, MASS (c), Dai L., Nakajima T.,
RL20_MYCPU HV41_WOUSE NU3M_SARGL NU3M_METSE RL20_THETN LCA_MACRG V124_ASFB7 V125_ASFL5 V125_ASFL5 CU24_ARADI CU26_ARADI	ALIGNMENTS	PRT; 30 AA	sequence update) annotation updat ta; Zygomycetes;	SEQUENCE. MEDLINE=79107453; PubMed=761621; Bradley W.A., Somkuti G.A.; "The primary structure of sillucin and antimic Mucor pusillus."; FEBS Lett. 97:81-83(1979)!- FUNCTION: Sillucin is an antimicrobial age the control of the control of sillucin is an antimicrobial age and the control of sillucin is an antimicrobial age the control of sillucin is an antimicrobial age and sillucin is an antimicrobial age of sorting and control of sillucin sillucin in a sefective and sillucin silluci	bonds are present.	; Score 24; DB %; Pred. No. 59 0; Mismatches		T; 38 A not update ation update ation update chelicerat rothele.  LOCATION, S. S. 4;
61.5 61.5 61.5 61.5 61.5 61.5 61.5 61.5		STANDARD; (Rel. 01, Crea	(Kel. 01, Last (Rel. 08, Last unsillus. 'ungi; Zygomyco	7453; PubMed=7, Somkuti G.A., Somkuti G.A., structure of us."; 81-83(1979). 3; Sillucin is nilic fungus rh	lism. our disulfide boo 0; SNUMP. 30 AA; 3209 MW	61.5% milarity 100.0 Conservative	2 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	STANDAE  1. 42, 1. 42, 1. 42, 1. 42, 1. 42, 1. 42, 1. 60,
44 4 2 2 2 4 4 4 4 2 4 4 4 4 4 4 4 4 4		T 1 RHIPU SILU RHIPU PO2885; 21-JUL-1986	21-UUL-1986 S1-UUL-1988 S1-IUCin. Rhizomucor F Eukaryota; Rhizomucor. NCBI_TaxID=4	MEDLINE=7910 Bradley W.A. The primary Wucor pusill FEBS Lett. S -! - FUNCTION	metaboli. -!- PTM: Fou PIR; A03380; Antibiotic. SEQUENCE 3	Query Match Best Local Sim: Matches 3;	1 GYW     18 GYW	AGGS 8357 0-0CT-200 0-0CT-
<b>ოოოოო</b>		RESULT SILU R 1D S AC P DT 2	444888888	14 X X X X X X X X X X X X X X X X X X X	855 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	A B A	Oy QD	RESULT TXXXXI TXXXXI TXXXXI TXXXXI TXXXXI TXXXXI TXXXI TXXXI XXXXI XXXI XXXXI XXXXI XXXXI XXXXI XXXXI XXXXI XX

Fri May

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                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complex.";
J. Bacteriol. 175:4699-4711(1993).
J. Bacteriol. 175:4699-4711(1993).
J. Bacteriol. 175:4699-4711(1993).
J. Bacteriol. 175:4699-4711(1993).
J. FUNCTION: HMWC (high-molecular-weight cytochrome c), ORF2, ORF3,
ORF4, ORF5 and ORF6 in the HMC operon form a transmembrane protein complex that allows electron flow from the periplasmic hydrogenase to the cytoplasmic enzymes that catalyze reduction of sulfates.
J. SUBCELLULAR LOCATION: Integral membrane protein.
                                                Spermatophyta; viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4081;
                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=cv. VFWT Cherry 1A1221;
MEDLINE=9424622; PubMed=7514532;
MEDLINE=9424622; PubMed=7514532;
Vera A., Sugiura M.;
"A novel RNA gene in the tobacco plastid genome: its possible role in the maturation of 185 rRNA.";
the maturation of 185 rRNA.";
EMBO J. 13:2211-2217(1994).
-1- SIMILARITY: Belongs to the 132P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=NCIME 83333, MEDLINE=93328674; PubMed=8335628; Repsil M., Pollock W. NB.R., Reij M.W., Keon R.G., Fu R., Voordouw G.; Rossi M., Pollock W.B.R., Reij M.W., Keon R.G., Fu R., Voordouw G.; Hithe hmc operon of Desulfavibrio vulgaris subsp. vulgaris Hildenborough encodes a potential transmembrane redox protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FBE-1994 (Rel. 28, Created)
01-FBE-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
5.8 kDa protein in HMC operon (ORF 4).
Beaulfoubiro vulgaris (etrain Hildenborough).
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfoubironales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.5%; Score 24; DB 1; Length 44; 100.0%; Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 AA; 5214 MW; 80314CF1400BAC0A CRC64;
Chloroplast 50S ribosomal protein L32 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Prec. ... o; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D17805; BAA04629.1; -.
PIR; T07762; T07762.
HAMAPP: MP 00340; -! 1.
InterPro IPR00267; Ribosomal_L32p.
Pfam; PF01783; Ribosomal_L32p; 1.
Ribosomal protein; Chloroplast.
                                         ycopersicon esculentum (Tomato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HMC4_DESVH
P333<u>9</u>1;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The structures of the major peptide toxins from the venom of the spider Macrothele gigas that bind to sites 3 and 4 in the sodium channel...;

Sodium channel...;

FEBS Lett. 547:43-50(2003).

-I. FUNCTION: Insecticidal neurotoxin. Induces flaccid paralysis when injected introlegiopteran larvae. Is not toxic to mice when injected intracranially at 20 pmol/g.

-I. TISSUE SPECIFICITY: Expressed by the venom gland.

-I. TISSUE SPECIFICITY: Expressed by the venom gland.

-I. MASS SPECIROMETRY: MM=4940.3; METHOD=MALDI.

-I. MASS LD (50) is 17.6 mmol/kg to lepidopteran larvae.

TOXIN: Neurotoxin; Sodium channel inhibitor; Ionic channel inhibitor.

SEQUENCE 40 AA; 4948 MW; 1B04FE5A35E31A96 CRC64;
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  "Distinct primary structures of the major peptide toxins from the venom of the spider Macrothele gigas that bind to sites 3 and 4 in the sodium channel.", FBBS Lett. 547:43-50(2003).
                                                                                     -!- FUNCTION: Insecticidal neurotoxin. Has no effect on lepidopteran larvae when injected at 20 pmol/g, or on mice when injected intracranially at 32.8 nmol/g, or on mice when injected intracranially at 32.8 nmol/g.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- PTW: Contains three disulfide bonds.
-!- PTW: Contains three disulfide bonds.
-!- MASS SPECIRONERY: WW-4563.0; METHOD=MALDI.
TOXIN; Neurotoxin; Sodium channel inhibitor; Ionic channel inhibitor.
SEQUENCE 38 AA; 4602 MW; F77D05A218675600 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-22744743; PubMed=12860384;
Corzo G., Gilles N., Satake H., Villegas E., Dai L., Nakajima T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neurotoxin Magi 2.
Macrothele gjas (Spider).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Mygalomorphae; Hexathelidae; Macrothele.
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                                                                                                                                                                                                                                                                                                                  61.5%; Score 24; DB 1; Length 38; 100.0%; Pred. No. 74; o; Mismatches 0; Indels
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(Rel. 29, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0-00T-2003 (Rel. 42, Created)
0-00T-2003 (Rel. 42, Last sequence update)
0-00T-2003 (Rel. 42, Last annotation update)
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3, Conservative
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RK32_LYCES
ID RK32_LYCES
AC P36493;
DT 01-UNY-1994 (
DT 28-FEB-2003 (
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P83558;
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RESULT 3 TXM2\_MACGS

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TRANSMEM

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                                                                                                                                                                                                                          Bukaryca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702, 51350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; Caryophyllales, Amaranthaceae, Spinacia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES-B.rapa; Sond Y.; Smill Spin General databases. Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases. -!- SIMILARITY: Belongs to the L32P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                      SECOTES A, thallana; STRAIN=cv. Columbia;
MEDLINE=20039611; PubMed=10574454;
Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.;
"Complete structure of the chloroplast genome of Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 24; DB 1; Length 51;
Pred. No. 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 AA; 5930 MW; 0AC447B5EDED00F3 CRC64;
                                                   01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Chloroplast 50S ribosomal protein L32.
Arabidopsis thaliana (Mouse-ear cress), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P28804; Q9M3J3;
01-DEC-1992 (Rel. 24, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Chloroplast 50S ribosomal protein L32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.5%; Scor.
100.0%; Pred. No. >>,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam, Prules; Naccontage Ribosomal protein; Chloroplast.
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STRAIN=cv. Geant d'hiver, and cv. Monatol;
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InterPro; IPR002677; Ribosomal L32p.
Pfam; PF01783; Ribosomal L32p; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AP000423; BAA84435.1; -.
EMBL, Z26332; CAA81233.1; -.
PIR, S37208; S37208.
                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
28-FEB-2003 (Rel. 41, Last ann
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Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Res. 6:283-290(1999).
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                                                                                                                                                                                                 Brassica rapa (Turnip)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
The 3; Conserva
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RK32_SPIOL
ID_RK32_S
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

EMBL; L16784; AAA71997.1; ---
PIR; D40605; D40605.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=Accession MG-20;
MEDLINE=21082929; Pubmed=11214967;
MEDLINE=21082929; Pubmed=11214967;
MEDCINE=21082929; Pubmed=11214967;
MCOMPlete structure of the chloroplast genome of a legume, Lotus japonicus.";
Japonicus.";
DNA Res. 7:323-330(2000).
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                                                                                                                                                                                                                                                                                                                                                Length 47;
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                                                                                                                                                                                                                                                           POTENTIAL.
30D4C1585B3C7209 CRC64;
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100.0%; Pred. No. 91;
tive 0; Mismatches
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28-FEB-2003 (Rel. 41, Last annotation update)
Chloroplast 50S ribosomal protein L32.
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InterPro; IFR002677, Ribosomal_L32p.
Pfam, PF01783, Ribosomal_L32p, 1.
Ribosomal_protein; Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AP002983; BAB33243.1; -.
                                                                                                                                                                                                                                                           18 37
47 AA; 5773 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 AA; 5844 MW;
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Thes 3; Conservative
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28-FEB-2003 (Rel. 41,
28-FEB-2003 (Rel. 41,
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Best Local Similarity
3, Conserve
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                                                                                                                                                                                                                                      Transmembrane.
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ID RK32_ARATH
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SEQUENCE

RESULT 7

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Gaps

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61.5%; Score 24; DB 1; Length 62; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels

62 AA; 7359 MW; 2034EF11BA2D0088 CRC64;

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PROSITE, PS00214; FABP; FALSE NEG.
Vitamin A; Retinol-binding; Transport.
                                                                                                                                                                 Query Match
Best Local Similarity 100.(
Matches 3; Conservative
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SEQUENCE
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                                                                                                                                                                                                                                                        STRAIN-CV. Alwaro;

MEDLINE=93043036, PubMed=1421149;

MEDLINE=93043036, PubMed=1421149;

MEDLINE=93043036, PubMed=1421149;

RT Porteins=schedence that organelle ribosomal procein genes are unctional and that NH2-terminal processing occurs via multiple pathways in chloroplasts.

Plant Mol. Biol. 20:459-465(1992).

RT Plant Mol. Biol. 20:459-465(1992).

C --- SIMILARITY: Belongs to the L32P family of ribosomal proteins.

C --- SIMILARITY: Belongs to the L32P family of ribosomal proteins.

C --- SIMILARITY: Belongs to the L32P family of ribosomal proteins.

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C --- SIMILARITY: Belongs to the L32P family of ribosomal proteins on the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way of modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/correct of the Lagonal Parkon Commercial entities requires a mail to license daysement (see http://www.isb-sib.ch/announce/correct of the Lagonal Parkon Commercial entities requires a mail to license daysement (see http://www.isb-sib.ch/announce/correct of the Lagonal Parkon Commercial entities requires a license daysement (see http://www.isb-sib.ch/announce/correct of the Lagonal Parkon Commercial entities requires a license daysement (see http://www.isb-sib.ch/announce/correct of the Lagonal Parkon Commercial entities requires and the Lagonal Parkon Commercial entities and commercial entities the commercial entities and commercial entities and commercial entities and commercial entitles and commercial entitles and commercial entitles and commercial entitles and commerc
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MEDLINE=20205626; PubWed=10725366;

MEDLINE=20205626; PubWed=10725366;

Merch P.J.L., Roell B., van Aalten D.M.F., de Jong W.W.;

Mecko iota-crystallin: how cellular retinol-binding protein became an eye lens ultraviolet filter.";

Proc. Natl. Acad. Sci. U.S.A. 97:3282-3287 (2000).

From Natl. Acad. Sci. U.S.A. 97:3282-3287 (2000).

-!-FUNCTION: BINDS VITAMIN A2 IN THE EYE LENS AND THUS FUNCTIONS AS A UV FILTER. INTRACELLULAR TRANSPORT OF RETINOL.

-I-SIMILARITY: Belongs to the fatty-acid binding protein (FABP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Gekkota, Gekkonidae, Gonatodes.
NCBI_TaxID=104610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                            Schmitz-Linneweber C., Maier R.M., Alcaraz J.-P., Cottet A., Herrmann R.G., Mache R.; "The plastid chromosome of spinach (Spinacia oleracea): complete nucleotide sequence and gene organization."; Plant Mol. Biol. 45:307-315(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.5%; Score 24; DB 1; Length 56; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 25 W -> S (IN REF. 2).
56 AA; 6504 MW; ACBA68500D9B49D5 CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Iota-crystallin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 AA.
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INTERFYC; IPROU0566; Lipocln_cytFABP.
Pfam; PF00061; lipocalin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAMAP; MF_00340; -; 1.
InterPro, Intro02677; Ribosomal_L32p.
Pfam; PF01783; Ribosomal_L32p; 1.
Ribosomal protein; Chloroplast.
   MEDLINE=21187424; PubMed=11292076;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ400848; CAB88781.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Conservative
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Best Local Similarity
Matches 3; Conserv?
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P82980; 1GGL.
                                                                                                                                                                                                                              SEQUENCE OF 1-29
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                    Projan S.J., Kornblum J., Kreiswirth B., Moghazeh S.L., Eisner W.,
Novick R.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
19.9sis procein S homolog from lambdoid prophage DLP12.
ESSD OR B0554 OR C1561.
ESCHORIA coll, and
Escherichia coli 06.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                             'Nucleotide sequence: the beta-hemolysin gene of Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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100.0%; Pred. No. 1.3e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 AA; 8207 MW; 77B8013E40A76839 CRC64;
                                                                                                                                                                                                       Staphylococcus aureus.
Bacteria, Firmicutes; Bacillales; Staphylococcus.
                                                                                              01-MaY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
16-077-2001 (Rel. 40, Last amotation update)
Hypothetical protein in hlb 3'region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 17:3305-3305(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; SIS767; SIS767.
InterPro; IPRO05830; Aer hem leuk.
InterPro; IPRO01340; Hemlysn_pore.
Pfam; PF01117; Aerolysin; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89263748; PubMed=2726469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X13404; CAA31770.1; -.
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Best Local Similarity 100....
                                                      STANDARD;
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                                                                                                                                                                                                                                                   NCBI_TaxID=1280;
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ESSD_ECOLI
ID ESSD_ECOLI
AC P77242;
RESULT 10
YHLB STAAU
ID YHLB STAAU
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MEDLINE=91210180; PubMed=2019562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
Federspiel N., Hyman R., Kalman S., Komp C., Kuxdi O., Lew H., Lin D.,
Namath A., Oeffner P., Roberts D., Schraum S., Davis R.W.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                       SEXURNE FROM N.A. A. STOCT 700928;

MEDLINE=22388234; PubMed=12471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P., Rasko D., Burland V., Plunkett G. III, Redford P., Rackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete genome sequence of urcopathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                              STRAIN=K12 / MG1655,
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMed=9278503;
MEDLINE F.R., PubMett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriophage P21 (Bacteriophage 21).
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
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InterPro, IPR007054, Lysis_S.
Pfam: PR04971, Lysis_S.
Hypothetical protein, Page lysis protein; Complete proteome.
SEQUENCE 71 AA, 7778 MM; 9C013E2FE4361843 CRC64;
                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.5%; Score 24; DB 1; Length 71;
100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0; Indels
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01-AUG-1992 (Rel. 23, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
 Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 217992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000161; AAC73655.1; -...
EMBL; U82598; AAB40750.1; -...
EMBL; AE016759; AAN80030.1; -...
PIR; H64787; H64787
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                                            SEQUENCE FROM N.A.
STRAIN≃K12 / MG1655;
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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P27360;
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SEQUENCE FROM N.A.

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MEDILINE=97061201; PubMed=8905231;
MEDILINE=97061201; DubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
Tabara S.,
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Bonovich M.T., Young R., "Dual start motif in two lambdoid S genes unrelated to lambda S.", J. Bacteriol. 173:2897-2905(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96127529; PubMed=8590279; Kotani H., Sazuka T., Miyajima N., Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N., Sugiura M., Tabata S.; Sugiura M., Tabata S.; Sequence analysis of the genome of the unicellular cyanobacterium "Sequence analysis of the genome of the unicellular region From positions 64% to 92% of the genome."; In the 1 Mb region from map positions 64% to 92% of the genome.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                       61.5%; Score 24; DB 1; Length 71; 100.0%; Pred. No. 1.4e+02; tive 0; Mismatches 0; Indels
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Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBL_TaxID=1148;
                                                                                                                                                                                                                                                                                     EMBL; M65239; AAA32349.1; -.
InterPro; IPR007054; Lysis_S.
Fam; PF04971; Lysis_S; 1.
Phage lysis protein.
SEQUENCE 71 AA; 7893 NW; 8690A8F25234A3E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein ss10738.
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ID Y738 SYNY3
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01-AUG-1991 (Rel. 19, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
Membrane protein UL43 homolog (ORF1) (Fragment).
Equine herpesvirus type 4 (strain 1942) (EHV-4) (Equine herpesvirus type 1 subtype 2).
                                                                                                                                                                                                                                                                                                                          Vaccinia virus (strain Copenhagen).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P., Paoletti E.; "Appendix to 'The complete DNA sequence of vaccinia virus'."; virology 179:517-563(1990).
                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91021027; PubMed≈2219722;
Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 61.5%; Score 24; DB 1; Length 74; Similarity 100.0%; Pred. No. 1.4e+02; 3; Conservative 0; Mismatches 0; Indels
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Hypothetical protein.
SEQUENCE 74 AA; 9485 MW; 0EAIDC187A16BE10 CRC64;
InterPro, IPR005357; UPF0150.

Byam; PF03681; UPF0150; 1.

Bypothetical proctein; Complete proteome.

SEQUENCE 72 AA, 7719 NW; 388310F96C0BE629 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete DNA sequence of vaccinia virus."; Virology 179:247-266(1990).
                                                                                                                                                                                                                                            01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 9.5 KDa protein.
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UL43_HSVE4
ID UL43_HSVE4
AC P22597;
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                                                                                                                                                                                                                                                                                   Virology 179:378-387(1990).
-!- SUBCELLULAR LOCATION: Membrane-associated or transmembrane protein
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-!- SIMILARITY: BELONGS TO FAMILY THAI GROUPS TOGETHER HSV-1 UL43,
EHV-1 17, AND VZV 15.
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                        Alphaherpesvirinae, Varicellovirus.
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PIR; A45343, A45343.
Interbro; IPR007764; Herpes UL43.
Pfam; PF05072; Herpes_UL43; 1.
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MEDLINE=91021040; PubMed=2171212;
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090UT7;
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090UT7
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"Phylogeny of the Asteridae s.l. based on sequences from four
different genes.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
BMBL, AN2362B1 CAB65471.1;
GO, GO:00005507; C:chloroplast; IEA.
GO; GO:0001637; F:NDBJ dehydrogenase (ubiquinone) activity; IEA.
GO; GO:0006120; F:matcochondictaes activity; IEA.
GO; GO:0006120; F:matcochondictal electron transport, NADH to u. .; IEA.
InterPro; IPR001750; Oxidored_q1.
InterPro; IPR001750; Oxidored_q1.
InterPro; IPR0011516; Oxidored_q1.
InterPro; IPR0011516; Oxidored_q1.
InterPro; IPR0011516; Oxidored_q1.
InterPro; IPR0011516; Oxidored_q1.
Pfam: PF00161 cxidored_q1.
                                                                                                                                                                                                                      DeBella L.R., Scherzer M., Wood S.;
DeBella L.R., Scherzer M., Wood S.;
DeBella L.R., Scherzer M., Wood S.;
Identification of a novel human gene (GOR) localized to 8q13-8q22.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AR02869; AAC98149.1;
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0004527; P:exonuclease activity; IEA.
Interpro, IPR066055; Exonuclease.
Pfem; PF00929; Exonuclease.
NON_TER
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Tropaeolaceae, Tropaeolum.
NCBI_TaxID=4020;
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                                                                                                            Homo sapiens (Human)
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Euteria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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170 AA; 19433 MW; 079DE87451B22A1B CRC64;
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01-MAY-1999 (TrEMBirel 10, Created)
01-MAY-1999 (TrEMBirel 10, Last sequence update)
01-UIM-2003 (TrEMBirel 24, Last annotation update)
GOR antigen (Fragment).
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MEDIATRS—9601284; PubMed=7559877;

MEDIATRS—9601284; PubMed=7559877;

Onnisht T., Arita N., Hayakawa T., Sato B., Kishimoto T., Onnisht T., Arita N., Hayakawa T., Sato B., Kishimoto T.,

"Identification of alternatively spliced messenger ribonucleic acid
encoding truncated growth hormone-releasing hormone receptor in human
pituitary adenomas.",

J. Glin. Endocrinol. Metab. 80:2933-2939(1995).

MON_TER.

NON_TER.
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MEDILTRE-29239477; PubbMed=1627586;
Singhal S.S., Saxena M., Ahmad H., Awasthi Y.C.;
"Glutathione S-transferase of mouse liver: sex-related differences in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0, Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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shochim. Blophys. Acta 1117:105-105(1992).
HSSP; P04905; 2GST.
SEQUENCE 15 AA; 1754 MW; 0284DB620E166ED4 CRC64;
                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEXBLrel. 10, Last annotation update)
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01-MAY-2000 (TrEMBirel. 13, Last sequence update)
01-OCT-2000 (TrEMBirel. 15, Last annotation update)
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                                                                                                                                                                   GHRH-R protein (Fragment). GHRH-R.
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PRELIMINARY;
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Nishinaka T., Yasunari C., Abe A., Nanjo H., Terada T., Nishihara T., Mizoguchi T.; Mizoguchi T.; "Comparison of purified lens glutathione S-transferase isozymes from rabbit with other species."; Curr. Eye Res. 12:333-340(1993).
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O1-MAY-2000 (TERMELRE). 13, Created)
O1-MAY-2000 (TERMELRE). 13, Last sequence update)
O1-MAY-2000 (TERMELRE). 15, Last annotation update)
O1-OCT-2000 (TERMELRE). 15, Last annotation update)
Glutathione S-transferase class MU PI7.8 isozyme (Fragment).
Oryctolagus cumiculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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Oryctolagus cuniculus (Rabbit).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Class MU glutathione S-transferase isozyme R11, class MU GST-RL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLINIONE 52213177; PubMed=8460849;
Priniano T., Novak R.F.;
"Purification and characterization of class mu glutathione transferase isozymes from rabbit hepatic tissue.";
Arch. Biochem. Biophys. 301:404-410(1993).
HSSP; P04905; 6GSU.
SEQUENCE 20 AA; 2316 MW; 7F5AC2468150E207 CRC64;
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Similarity 100.0%; Pred. No. 3.4e+02;
3; Conservative 0; Mismatches 0; Indels
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                                                                                             SEQUENCE FROM N.A.

Poux C., van Rheede T., Madsen O., de Jong W.W.;

"Sequence gaps join mices and men.";

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ438199; CAD27283.1;

NON TER
                                                                                                                                                                                                                                                                                     SEQUENCE 17 AA; 1995 MW; 05B9D808B11C40C3 CRC64;
Mammalia; Eutheria; Insectivora; Talpidae; Talpa.
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Best Local Similarity 100...
3; Conservative
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Best Local Similarity
Matches 3; Conserva
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                                         NCBI_TaxID=9375;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10118;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                       Sciurus vulgaris (Red squirrel).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Sciuridae, Sciurinae,
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"Electrospray ionization-mass spectrometry as a tool for characterization of glutathione S-transferase isozymes.";
Mal. Biochem. 229:304-312 (1995).
GO: 00:0004364; F:glutathione transferase activity; IEA.
SEQUENCE 15 AA; 1701 MM; 9A54C712143F7C4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Poux C., van Rheden T., Madsen O., de Jong W.W.;
Poux C., van Rheden T., Madsen O., de Jong W.W.;
Suduence gaps join mices and men.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ438202; CAD27287.1; -.
NON TER
SEQÜENCE 15 AA; 1723 MW; 5E28E8178B86161E CRC64;
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01-00T-2002 (TrEMBLrel. 22, Last sequence update)
01-00T-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                          01-00T-2002 (TrEMBLrel. 22, Last sequence update) 01-0CT-2002 (TrEMBLrel. 22, Last annotation update) Prion protein (Fragment).
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MEDLINE=96036981; PubMed=7485987;
                                                                                                                  01-OCT-2002 (TrEMBLrel. 22,
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Best Local Similarity
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Q9QUL8;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
MU class glutathione S-transferase subunit 6 (EC 2.5.1.18) (Fragment).
Rattus sp.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10095;
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MEDLINE=93183007; PubMed=8442656;
Awasthi S., Singhal S.S., Srivastava S.K., Awasthi Y.C.;
Awasthi S., Singhal S.S., Srivastava S.K., Awasthi Y.C.;
Awasthi S., Singhal S.S., Srivastava S.K., Awasthi Y.C.;
Arburification and characterization of glutathione S-transferase (murine ovary and testis.";
Arch. Biochem. Biophys. 301:143-150(1993).
Arch. Biochem. Biophys. 301:143-150(1993).
Arch. Biochem. 4GTU.
GO:00004644; F:Qlutathione transferase activity; IEA.
GO:00046464; F:Qlutathione transferase activity; IEA.
Aravinda S., Gopalakrishnan B., Dey C.S., Totey S.M., Pawshe C.H.. Salunke D., Kaur K., Shaha C.;
Salunke D., Kaur K., Shaha C.;
A testicular protein important for fertility has glutathione S-transferase activity and is localized extracellularly in the seminiferous tubules..;
J. Biol. Chem. 270:15675-15685 (1995).
HSSP; Q03013; 4GTU.
GO; GO:0004364; F:glutathione transferase activity; IEA.
SEQUENCE 20 AA; 2344 MW; 7F5423EE224A54C7 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 24, Last annotation update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Glutathione S-transferase UZ subunit (EC 2.5.1.18) (Fragment).
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MEDLINE=96036981; PubMed=7485987;
MEDLINE=96036981; PubMed=7485987;
MEDLINE=96036981; PubMed=7485987;
"Electrospray ionization-mass spectrometry as a tool for characterization of glutathione S-transferase isozymes.";
Anal. Biochem. 229:304-312(1995).
HSSP; Q03013; 4GTU.
G0; G03004364; F:glutathione transferase activity; IEA.
SEQUENCE 20 AA; 2310 WW; 7F5AC3EE224A54C7 CRC64;
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3; Conservative 0; Mismatches 0;
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Q9QUL8
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTN-2003 (TrEMBLrel. 14, Last sequence update)
MU class glutathione S-transferase subunit 4 (BC 2.5.1.18) (Fragment).
Rattus sp.
Bukaryota, Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
MU class glutathione S-transferase subunit 3 (EC 2.5.1.18) (Fragment).
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10118;
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                                                                                                Primano T., Novak R.F.;
Purification and characterization of class mu glutathione transferace isozymes from rabbit hepatic tissue.";
Arch. Blochem. Blophys. 301:404-410(1993).
HIX, 530381; 530381.
HSSP; PS2161; HHNA.
SEQUENCE 20 AA; 2330 NW; 7F5AC25E2250E207 CRC64;
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Roulmi P., Debrauwer L., Tulliez J.;
"Blectrospray ionization-mass spectrometry as a tool for
characterization of glutathione S-transferase isozymes.";
Anal. Biochem. 229:304-312(1995).
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MEDLINES-96036981; PubMed=7485987;

Rouimi P., Debrauwer L., Tulliez J.;

"Electrospray ionization-mass spectrometry as a tool for

characterization of glucathione S-transferase isozymes.";

Anal. Biochem. 228:304-312(1995).

HSSP; Pod4905; 263.

GO; GO:0004964; F:glutathione transferase activity; IEA.

SEQUENCE 20 AA; 2363 MW; 3B4F19C689F2B4DB CRC64;
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Matches 3; Conservative 0; Mismatches 0; Indels
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SEQUENCE.
MEDLINE=95318156; PubMed=7797568;
                                                                MEDLINE=93213177; PubMed=8460949;
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O1-MAY-2000 (TEMBLE) 13, Created)

O1-MAY-2000 (TEMBLE) 13, Last sequence update)

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Glutathione S-transferase, GST (Fragment).

Rattus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Matches 3; Conservative 0; Mismatches 0; Indels
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7, 2004, 06:21:40 ; Search time 45.76 Seconds (without alignments) 49.396 Million cell updates/sec
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Run on:

Total number of hits satisfying chosen parameters: 1586107 segs, 282547505 residues Gapop 10.0 , Gapext 0.5 US-10-046-922-68 1 GYWXXXWX 8 **BLOSUM62XX** Perfect score: Scoring table: Searched: Sequence: Title:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match	Length	DB	ID	Description
-	39	100.0	. co	5	ABP53965	Abp53965 VEGFR-3 b
7	39	100.0	10	Ŋ	ABP53968	ADD53968 VEGFR-3 b
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15	26	66.7	46	9	ABU57807	Abu57807 HIV envel
16	26	66.7	46	ø	ABU57806	Abu57806 HIV envel
17		66.7	46	9	ABU57815	
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20	56	66.7	46	9	ABU57812	Abu57812 HIV envel
21	56	66.7	46	9	ABU57813	Abu57813 HIV envel
22	26	66.7	46	9	ABU57817	Abu57817 HIV envel
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## ALIGNMENTS

Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotenaive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor. VEGFR-3 binding peptide SEQ ID NO:68. ABP53965 standard; peptide; 8 AA. (first entry) 09-JAN-2003 ABP53965; ABP53965 ID APPE RESULT 1 

Location/Qualifiers Homo sapiens. Synthetic.

Misc-difference 4. .6 /note= "X is any amino acid" /note= "any amino acid" Misc-difference 8 WO200257299-A2 25-JUL-2002.

ï CANCER RES Kubo 17-JAN-2001; 2001US-0262476P. Alitalo K, Koivunen E, (LUDW-) LUDWIG INST ( (LICN ) LICENTIA LTD

16-JAN-2002; 2002WO-IB000099.

WPI; 2002-691521/74.

New isolated peptide that inhibits VEGP-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.

Claim 22; Page 81; 149pp; English.

The present invention describes an isolated peptide (I) that binds to and

Gaps

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100.0%; Score 39; DB 5; Length 10; 100.0%; Pred: No. 0.34; 1. No. 0; Mismatches 0; Indels

0; Mismatches

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have cytostatic, hepatotropic, antiinflammatory, hypotensive, antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for the call surface receptor VEGFR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, opanicraes, colon, stomach, brast, endometrium, prostate, testicle, oxary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, heamangiomas and diabetes. The present sequence represents a VEGFR-3 binding peptide, which is given in the exemplification of the present invention
inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
                                                                                                                                                                                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                              1 GYWXXXWX
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                                                                                                                                                                                                                                                      Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vinerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
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                  have cytostatic, hepatotropic, antiinilammatory, hypotensive, antidiabatic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, brast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
       inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                            Length
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100.0%; Pred. No. 1.4e+06;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEGFR-3 binding peptide SEQ ID NO:73.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP53968 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kubo H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CANCER RES
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Best Local Similarity 100.
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(LICN ) LICENTIA LTD.
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                                                                                                                                                                                                                      present invention
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                                                                                                                                                                                                                                                          Sequence 8 AA;
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and
                                                                                                             Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; unnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes an isolated peptide (I) that binds to inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive,
                                                                                                                                                                                                                                                                                                        /note= "X is any amino acid"
                                                                                       VEGFR-3 binding peptide SEQ ID NO:67.
                                                                                                                                                                                                                                                                         Location/Qualifiers
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ABP53964 standard; peptide; 7 AA.
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                                                          (first entry)
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Synthetic
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Best Local S
Matches 6
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antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of envokacularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
                                                                                                                                                                                                                                                                                                                                      CCR5, CC chemokine receptor 5; human; HIV infection; human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome; drug screening; identification; peptide library.
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                                                                                                                                            Length 7;
                                                                                                                                                              0; Indels
                                                                                                                                           97.4%; Score 38; DB 5; Le
100.0%; Pred. No. 1.4e+06;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                    CCR5-related peptide library CPI-10042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "Any amino acid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2000; 2000US-0190996P.
21-MAR-2000; 2000US-0191299P.
20-MAR-2001; 2001US-00813448.
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20-MAR-2001; 2001US-00813653
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                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                   1 GYWXXXW 7
                                                                                                                                                                                                GYWXXXW
                                                                                                      present invention
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                                                                                                                        Sequence 7 AA;
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                                                                                                                                                                                                                                                                                                 22-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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The invention relates to a method for identifying a binding compound for C chemokine receptor 5 (CCR5). The method involves screening a library C C chess molecules (particularly peptides) with immobilised CCR5, and then identifying those molecules which bind. The invention also relates to cCR5-binding molecules identified using the method of the invention. The invention also relates to cCR5-binding molecules identified using for CCR5-binding peptides, a transfer vector encoding tagged CCR5, a computer-aided methods for determining the relative binding assay that utilises the three-dimensional structure of CCR5. Compounds identified using the methods of the invention are useful for treating or preventing HIV (human immunodeficiency virus) infection or AIDS (acquired immunodeficiency or antagonists of the invention may also be used to identify agonists or antagonists of the interaction of CCR5 sith its natural ligand, and to determine a binding motif for CCR5. Sequences A the invention
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comprises binding a molecule from library to a molecule having binding property corresponding to CCR5 and identifying bound molecule.
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100.0%; Pred. No. 79;
ive 0; Mismatches C
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/note= "Other= any amino acid"
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                                                                                                Example 3; Page 27; 50pp; English.
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/label= OTHER
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6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-488470/53.
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                                                                                                The invention relates to a composition comprising a polymer that forms a dydrogel at physiclogical temperature and a T20 or T1249 polypeptide release of a peptide, especially T20 or T1249 in the treatment of survivolument and peptide, especially T20 or T1249 in the treatment of Huban immunodeficiency virus) infections and, in the case of T1249, SIV commission immunodeficiency virus) infections and, in the case of T1249, SIV room temperature and can be administered easily but form hydrogels at room temperature. This allows the polypeptide to be released with improved pharmacokineit properties and bloavallability with increased half-life and reduced clearance rates. The present sequence is a generic enhancer peptide sequence with may be used in a fusion peptide (in either orientation) with T20 or T1249 to enhance the pharmacokinetic properties of the resultant hybrid peptide
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Composition for sustained delivery of e.g. a polypeptide including T20 or T1249 comprises a polymer which forms a hydrogel at physiological temperature and is useful for treating HIV infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hiv infection, simian immunodeficiency virus; T20; T1249; AIDS; AGGULTEd immunodeficiency syndrome; SIV infection; Anti-HIV, virucide; Cytckine; reverse transcriptase inhibitor; viral mRNA capping inhibitor; hydrogel; enhancer peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition for sustained delivery of e.g., a polypeptide including T20 T1249 comprises a polymer which forms a hydrogel at physiological temperature and is useful for treating HIV infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-HIV enhancer peptide, generic peptide #11.
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                                                                     Disclosure; Page 13; 37pp; English
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                                          The invention relates to a composition comprising a polymer that forms a devicable at physiological temperature and a T20 or T1249 polypeptide derivative. Administration of the composition is designed for sustained release of a peptide, especially T20 or T1249 in the treatment of HIV (human immunodeficiency virus) infections and, in the case of T1249, SIV (simian immunodeficiency virus) infection. The compositions are liquid at room temperature and can be administered easily but form hydrogels at physiological temperature. This allows the polypeptide to be released with improved pharmacokinetic properties and bloavailability with increased half-life and reduced clearance rates. The present sequence is a generic enhancer poptide sequence which may be used in a fusion peptide (in either orientation) with T20 or T1249 to enhance the pharmacokinetic properties of the resultant hybrid peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the consensus sequence of enhancer peptides which may be linked to a core polypeptide to form a novel hybrid polypeptide. The hybrid polypeptide exhibits enhanced pharmacokinetic properties relative to those exhibited by the core polypeptide when introduced into a living system. It is used to increase the in vitro or ex vivo half-life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New hybrid polypeptide, useful for preventing, treating and diagnosing e.g. viral infections, comprises an enhancer peptide linked to a core polypeptide.
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              Disclosure; Page 13; 37pp; English
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Disclosure; Page 12; 37pp; English.

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of the core polypeptide. The hybrid and core polypeptides can be used for modulating fusogenic events and intracellular processes involving coiled-
coil peptide interactions. Other uses include preventing, treating and/or diagnosing disorders involving fusion events (e.g. modulation of neurotransmitter exchange and sperm-egg fusion), intracellular processes involving coiled-coil peptides (e.g. modulation) and viral infections that involve cell-cell and/or virus, respiratory syncytial infections caused by human immunodeficiency virus, respiratory syncytial infections caused by human immunodeficiency virus, respiratory syncytial virus. Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and polio virus). The enhancer peptide sequence increases the half-life and reduces the clearance rate of therapeutic peptides, which increases their efficacy and minimises the incidence and severity of adverse side efficacy and minimises the incidence and severity of the diagnostic procedure in which they are used. (Updated on 06-AUG-2003 to correct OS field.) (Updated on 11-SEP-2003 to standardise OS field)
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The hybrid polypeptide exhibits enhanced pharmacokinetic properties relative to those exhibited by the core polypeptide when introduced into a living system. It is used to increase the in vitro or ex vivo half-life of the core polypeptides can be used for
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